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(57) Abstract

Polypeptides and proteins comprising the CD2-binding domain of LFA-3 are disclosed. DNA sequences that code on expression for those polypeptides and proteins, methods of producing and using those polypeptides and proteins, and therapeutic and diagnostic compositions are also disclosed. Deletion mutants unable to bind CD2 and methods for their use are also disclosed. In addition, fusion proteins which comprise the CD2-binding domain of LFA-3 and a portion of a protein other than LFA-3, DNA sequences encoding those fusion proteins, methods for producing those fusion proteins, and uses of those fusion proteins are disclosed.

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CD2-BINDING DOMAIN OF LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN 3

This invention relates to DNA sequences encoding and polypeptides which comprise the CD2-binding domain of Lymphocyte Function Associated Antigen 3 ("LFA-3") and to recombinant DNA molecules for expression of those polypeptides. In accordance with this invention, unicellular hosts transformed with the DNA sequences and recombinant DNA molecules containing these DNA sequences may be prepared and used to produce proteins and polypeptides comprising the CD2-binding domain of LFA-3. The peptides, polypeptides and proteins of this invention are useful in the study of interactions between CD2 and LFA-3, in diagnostic and therapeutic compositions, in antibody screening or purification methods and in other methods of this invention.

BACKGROUND OF THE INVENTION

T-lymphocytes play a major role in the immune response by interacting with target and antigen presenting cells. T-lymphocyte-mediated killing of target cells is a multi-step process involving adhesion of cytolytic T-lymphocytes to target cells. The initiation of the immune response to most antigens involves adhesion of helper T-lymphocytes to antigen-presenting cells.

These interactions of T-lymphocytes with target and antigen-presenting cells are highly specific and depend on the recognition of an antigen on the target or antigen-presenting cell by one of the many specific antigen receptors on the surface of T-lymphocytes.

The receptor-antigen interaction of T-lymphocytes and other cells is facilitated by various T-lymphocyte surface proteins, e.g., the antigen-receptor complex CD3 and accessory molecules CD4, LFA-1, CD8 and CD2. The interaction of T-lymphocytes and other cells is also dependent on accessory molecules, such as ICAM-1, MHC class I and II and LFA-3, that are expressed on the surface of target or antigen-presenting cells and thereby play a role in the action of T-lymphocytes. One general hypothesis is that accessory molecules on the T-lymphocytes and on the target or antigen-presenting cells interact with each other to mediate intercellular adhesion. Accordingly, these accessory molecules are believed to enhance the efficiency of lymphocyte/antigen-presenting cell and lymphocyte/target cell interactions and to be important in cell adhesion-based pathologies (such as leukocyte/endothelial cell interaction leading to pathologic inflammation) and lymphocyte recirculation. Accessory molecules are also involved in activation of lymphocytes.

One important example of cell-cell interaction mediated by accessory molecules is the specific interaction between CD2 (a T-lymphocyte accessory molecule) and LFA-3 (a target cell accessory molecule). CD2/LFA-3 binding appears to be essential for many important cell-cell reactions, including the initiation of the T-lymphocyte functional responses (Dustin et al., J. Exp. Med., 165, pp. 677-92 (1987);

Springer et al., Ann. Rev. Immunol., 5, pp. 223-52 (1987)). The importance of the CD2/LFA-3 complex in cell-cell adhesion is indicated by the findings that purified LFA-3 binds to CD2 on the surface of T-lymphocytes (Dustin et al., J. Exp. Med., 165, pp. 677-92 (1987)), that CD2 purified from T-lymphocytes binds LFA-3 on cell surfaces and inhibits the binding of LFA-3-specific monoclonal antibodies ("MAbs") to LFA-3 (Selvaraj et al., Nature, 326, pp. 400-403 (1987)), and that rosetting of human erythrocytes, which express LFA-3, to cells expressing CD2 is blocked by anti-LFA-3 MAbs and anti-CD2 MAbs (see, e.g., Seed et al., Proc. Natl. Acad. Sci. USA, 84, pp. 3365-69 (1987)).

LFA-3, which is found on the surface of a wide variety of cells including monocytes, granulocytes, T-lymphocytes, erythrocytes, B-lymphoblastoid cell lines, thymic epithelial cells, and vascular endothelial cells, has become the subject of a considerable amount of study to further elucidate its role in various T-lymphocyte interactions. Two natural forms of LFA-3 have been identified. One form of LFA-3 ("transmembrane LFA-3") is anchored in the cell membrane by a transmembrane hydrophobic domain. cDNA encoding this form of LFA-3 has been cloned and sequenced (see, e.g., Wallner et al., J. Exp. Med., 166, pp. 923-32 (1987)). Another form of LFA-3 is anchored to the cell membrane via a covalent linkage to phosphatidylinositol ("PI")-containing glycolipid. This latter form has been designated "PI-linked LFA-3", and cDNA encoding this form of LFA-3 has also been cloned and sequenced (Wallner et al., PCT patent application WO 90/02181).

Although the DNA sequence of the LFA-3 gene and the primary amino acid sequences of both forms of

LFA-3 have been determined, the actual site of interaction between LFA-3 and its receptor, CD2, has not previously been identified. There is a need to identify the CD2-binding domain on LFA-3 in order to better understand the specific interaction between CD2 and LFA-3 and, thereby, to effect and modulate the cellular and immunological processes that are dependent on the formation of the CD2/LFA-3 complex. Such information would also be useful in a variety of other applications including diagnostic and therapeutic compositions, protein purification, antibody identification and purification, and comparative and structural studies of LFA-3 and other proteins.

SUMMARY OF THE INVENTION

This invention addresses the aforementioned needs by identifying the CD2-binding domain of LFA-3 and providing nucleotide sequences defining the CD2-binding region of LFA-3 and CD2 binding polypeptides encoded by those sequences. The present invention provides polypeptides having the amino acid sequence: X_1-X_2-(SEQ ID NO:1) Asn Arg Val Tyr Leu Asp Thr Val Ser Gly-Y, wherein:

X_1 is hydrogen or methionyl;

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy terminal 1 to 77 amino acids of the sequence (SEQ ID NO:5): Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino-terminal 1 to 32 amino acids of the sequence (SEQ ID NO:33): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val;

and analogs and derivatives thereof,

said polypeptides being capable of binding to CD2.

In another embodiment, the present invention provides polypeptides having the amino acid sequence: X_1-X_2-(SEQ ID NO:1) Asn Arg Val Tyr Leu Asp Thr Val Ser Gly-Y, wherein:

X_1 is hydrogen or methionyl;

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy-terminal 1 to 50 amino acids of the sequence (SEQ ID NO:2): Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino-terminal 1 to 10 amino acids of the sequence (SEQ ID NO:3): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser;

and analogs and derivatives thereof,

said polypeptides being capable of binding to CD2.

The invention also provides DNA sequences encoding the above polypeptides, recombinant molecules containing those DNA sequences, hosts transfected with such DNA sequences and molecules and methods of making the polypeptides recombinantly, synthetically or semi-synthetically.

The polypeptides of this invention are useful in diagnosing diseases characterized by the presence or absence of CD2 on the surface of particular cells and to treat pathologies dependent on the formation of the LFA-3/CD2 complex.

The polypeptides of this invention and the DNA sequences encoding them may also be used to prepare recombinant or synthetic fusion proteins, which comprise a functional CD2-binding domain or polypeptide of LFA-3, as defined above, and another domain of a protein or polypeptide other than LFA-3. The CD2-binding domain portion of the fusion proteins allows the other polypeptides to be targeted specifically to CD2-expressing cells ($CD2^+$ cells). DNA sequences encoding these fusion proteins are also part of this invention.

One example of such fusion proteins of this invention is novel fusion proteins containing a portion of LFA-3 containing a functional CD2-binding domain, as defined above, fused to at least a portion of the Fc region of an immunoglobulin (Ig). Unexpectedly, the LFA-3-Ig fusion proteins of this invention inhibit T-lymphocyte activation and proliferation of peripheral blood lymphocytes.

It is a further aspect of this invention that the polypeptides and fusion proteins of this invention may also be used to label CD2 molecules, for example, soluble CD2, in solution or on the surface of T-lymphocytes or other CD2-expressing cells. The polypeptides and fusion proteins of this invention may also be used to label any protein, polypeptide or peptide comprising the domain of CD2 which binds LFA-3, for example, in a fusion protein generated using recombinant DNA techniques.

The polypeptides and fusion proteins of this invention may also be used in affinity chromatography to purify CD2 or any other polypeptide or protein conjugate containing the domain of CD2 which binds LFA-3.

This invention also provides altered (mutant) forms of the LFA-3 protein which lack the CD2-binding domain and the DNA sequences encoding such "deletion mutant" forms of LFA-3. Mutant proteins, which lack the CD2-binding domain of LFA-3, as defined above, may be used *in vivo* or *in vitro* to generate or to bind antibodies or other molecules that recognize epitopes or sites on LFA-3 other than the CD2-binding domain.

In addition to the monomeric form of the CD2-binding polypeptides and fusion proteins of this invention, multimeric forms are also enabled by this invention. Such forms may have enhanced affinity for CD2, enhanced immunogenicity and/or enhanced ability to initiate T-lymphocyte functional responses, e.g., stimulation of T-cell activation, through more effective or multiplied formation of CD2/LFA-3 complexes. Also, such multimeric forms may be more effective in competitive binding of CD2, making them more useful as immunosuppressants and more sensitive as diagnostics or reagents.

In addition, this invention contemplates antibodies recognizing the polypeptides and fusion proteins of this invention. Polyclonal and monoclonal antibodies to the polypeptides and fusion proteins of this invention may be obtained by immunizing an animal with polypeptides or fusion proteins of this invention.

Low molecular weight (generally less than 1000 daltons) inhibitors of the formation of the CD2/LFA-3 complex are also provided by this invention. Such "small molecule" inhibitors may be produced *in*

vitro by synthetic methods and may comprise part of the amino acid sequences of the polypeptides of this invention or may be entirely non-peptidyl organic molecules having a structural conformation that is able to mimic the binding specificity of the polypeptides and fusion proteins of this invention to CD2.

This invention also provides methods, compositions and kits for diagnostic and therapeutic uses in which the presence or absence of the CD2-binding domain of LFA-3 is desirable.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 (Fig. 1A and Fig. 1B taken together) depicts amino acid (SEQ ID NO:10) and nucleotide (SEQ ID NO:9) sequences of transmembrane LFA-3 indicating (with underlining) deletions made in the extracellular region of LFA-3. Regions designated M53, M54, M55, M56, M57, M58, M59, M60, M61, M62, M63, M64, M65, M66, M90, M91 and M92, respectively, were looped out to create recombinant genes encoding 17 separate deletion mutants. Expression of the deletion mutants in mammalian cells provided altered LFA-3 surface proteins missing a segment of amino acids present in the native LFA-3 protein. For example, expression of the deletion mutant designated M57 (that is, the LFA-3 DNA of Fig. 1 having the M57 region deleted) in CHO cells resulted in a mutant LFA-3 that did not bind to CD2. The amino terminal methionine (Met) is designated -28 to indicate that it is the amino terminal residue of the 28-amino acid signal peptide sequence of preLFA-3. The amino terminal residue of mature LFA-3 is a phenylalanine (Phe) and is designated +1.

Figure 2 (Figs. 2A, 2B, 2C, 2D, 2E, 2F, 2G, 2H, 2I, 2J, 2K, 2L, 2M and 2N taken together) depicts results of immunofluorescence flow cytometry by FACS

analysis of transfected CHO cells expressing mutant forms of LFA-3 encoded by deletion mutants M57 (Figs. 2A and 2B), M65 (Figs. 2C and 2D), M63 (Figs. 2E and 2F), M54 (Figs. 2G and 2H), M55 (Figs. 2I and 2J), M56 (Figs. 2K and 2L), and M58 (Figs. 2M and 2N). Transfected cells were reacted with anti-LFA-3 polyclonal antiserum 202 (dashed lines, Figs. 2A, 2C, 2E, 2G, 2I, 2K, 2M), anti-LFA-3 MAb TS2/9 (dashed lines, Figs. 2B, 2D, 2F, 2H, 2J, 2L, 2N), or anti-LFA-3 MAb 7A6 (dotted lines, Figs. 2B, 2D, 2F, 2H, 2J, 2L, 2N). In each analysis, the control peak (solid line) represents the cell population with background levels of fluorescein isothiocyanate-conjugated (FITC) goat anti-mouse or goat anti-rabbit IgG binding.

Figure 3 (Figs. 3A, 3B and 3C taken together) depicts the results of a Jurkat cell binding experiment. The photomicrographs show Jurkat cells expressing CD2 mixed with normal CHO cells (negative control) (Fig. 3A), M57/CHO cells (Fig. 3B) and P24/CHO cells expressing PI-linked LFA-3 (positive control) (Fig. 3C).

Figure 4 depicts a Northern gel analysis of LFA-3 gene transcripts synthesized in M57/CHO cells. Filters containing mRNA samples from CHO negative control cells (lane 1), M57/CHO cells (lane 2) and M16.3/CHO positive control cells (lane 3) were probed with a NotI restriction fragment of plasmid pLFA3M54, containing nucleotides 1-153 and 184-1040 of the LFA-3 cDNA sequence (see Figure 1), labeled with ^{32}P by nick-translation.

Figure 5 shows an autoradiogram depicting the differential immunoprecipitation of proteins from ^{125}I surface-labeled M57/CHO cells (lanes 1-4), normal CHO cells (negative control)(lanes 5-7), and P24/CHO cells (positive control)(lanes 8-11). Lysates of surface-

labeled cells were reacted with anti-LFA-3 MAb TS2/9 (lanes 2, 5, 9), anti-LFA-3 MAb 7A6 (lanes 3, 6, 10), or anti-LFA-3 polyclonal antiserum 202 (lanes 4, 7, 11). The antibody-precipitated proteins were electrophoresed on SDS-polyacrylamide gels prior to autoradiography.

Figure 6 (Figs. 6A and 6B taken together) depicts amino acid (SEQ ID NO:10) and nucleotide (SEQ ID NO:9) sequences of transmembrane LFA-3 indicating (with underlining) deletions in the extracellular region of LFA-3. Regions designated M100, M101, and M102, respectively, were looped out to create recombinant genes encoding 3 separate deletion mutants.

Figure 7 (Figs. 7A, 7B, 7C and 7D taken together) shows results of Jurkat cell-binding experiments in which Jurkat cells expressing CD2 were mixed with (a) normal CHO cells, (b) M100/CHO cells, (c) M101/CHO cells, or (d) M102/CHO cells.

Figure 8 (Figs. 8A, 8B and 8C taken together) shows Jurkat cell binding by LF08/AffiGel-10 beads (see Example 8, infra). LF08/AffiGel-10 beads were mixed with Jurkat cells and the cell-bead binding observed under a microscope (Figs. 8A and 8B). For comparison (negative control), a non-LFA-3 peptide from hepatitis B (i.e., "MXC 01", (SEQ ID NO:4) Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Val Val Asp Val Val Arg Asn) was fixed to Affigel-10 beads, the beads mixed with Jurkat cells, and cell-bead binding recorded in Fig. 8C.

Figure 9 depicts the amino acid (SEQ ID NO:12) and nucleotide (SEQ ID NO:11) sequences of PI-linked LFA-3 indicating (with underlining) the internal deletion made in the nucleotide sequence and corresponding mutant PI-linked LFA-3 protein. The region of the DNA designated PIM3 was looped out to

create a recombinant gene encoding a mutant protein containing the N-terminal 89 amino acids of PI-linked LFA-3 but lacking the subsequent 71 amino acids. Expression of the deletion mutant PIM3 (that is, the PI-linked LFA-3 DNA of Fig. 9 having the PIM3 region deleted) in CHO cells resulted in a mutant form of PI-linked LFA-3 that retained a CD2-binding domain.

Figure 10 (Figs. 10A and 10B taken together) depicts results of immunofluorescence flow cytometry by FACS analysis of transfected CHO cells expressing a mutant form of PI-linked LFA-3 encoded by deletion mutation PIM3. Transfected cells (PIM3.25.2 cells) expressed a surface protein that was recognized by anti-LFA-3 MAb TS2/9 (Figure 10A, dashed line) and that was susceptible to release from the cell surface by PI-PLC treatment (Figure 10A, dotted line). Figure 10B depicts the results of a similar analysis using transfected CHO cells amplified for expression of the mutant PI-linked protein (PIM2.25.2.100.12 cells). These cells produced a protein on their cell surface recognized by MAb 7A6 (Figure 10B, dashed line) and that was susceptible to release from the cell surface by PI-PLC treatment (Figure 10B, dotted line). In each analysis, the control peak (solid line) represents the cell population with background levels of FITC-conjugated goat anti-mouse IgG binding.

Figure 11 is a diagram of a dimer of LFA3TIP, depicting the various domains of this LFA-3-Ig fusion protein. As depicted in this figure, "LFA-3" refers to the amino terminal 92 amino acids of mature LFA-3. "H" refers to the ten amino acids of the IgG1 hinge region containing two cysteines to form two intermolecular disulfide bonds. Each disulfide bond is depicted as horizontal double SS. "C_H2" and "C_H3" refer to the two

constant domains present in the Fc region, below the hinge region, in human IgG1 molecules.

Figure 12 depicts the amino acid (SEQ ID NO:43) and nucleotide (SEQ ID NO:42) sequences of preLFA3TIP (i.e., LFA-3 (amino acids +1-+92) and the 28-amino acid signal sequence) and the various domains of the fusion protein. The nucleotide sequence of Figure 12 is also the same as the DNA sequence insert in the expression plasmid pSAB152.

Figure 13 is a photograph of a Western blot analysis of SDS-PAGE gels under nonreducing (lanes 1 and 2) and reducing (lanes 3 and 4) conditions. Lanes 1 and 3 are high molecular weight markers (BRL, Gaithersburg, Maryland). Lanes 2 and 4 contain LFA3TIP purified as described in Example 13.

Figure 14 (Figs. 14A and 14B taken together) depicts results of immunofluorescence flow cytometry by FACS analysis of Jurkat cells incubated with LFA3TIP plus R-Phycoerythrin conjugated anti-human IgG $F(ab')_2$ (dotted lines) in the presence of anti-CD2 MAb TS2/18 plus FITC conjugated goat anti-mouse IgG(H+L) $F(ab')_2$ (small dots in Fig. 14A) or anti-CD2 ascites fluid $T11_1$ (dashes in Fig. 14A), $T11_2$ (dashes in Fig. 14B) or $T11_3$ (small dots in Fig. 14B), plus FITC conjugated goat anti-mouse IgG(H+L) $F(ab')_2$.

Figure 15 depicts the results of a human allogeneic mixed lymphocyte reaction (MLR) assay for T-cell activation as measured by ^3H-thymidine incorporation into T-cells in the presence of anti-LFA-3 MAb 1E6 (closed squares), LFA3TIP (closed circles) and nonspecific human IgG1 (closed triangles).

Figure 16 depicts the results of MLR assays for inhibition of T-cell activation by selected proteins. "7A6" and "1E6" are anti-LFA-3 monoclonal antibodies (MAbs), specific for the CD2-binding domain

of LFA-3. "TS2/18" is an anti-CD2 MAb. "LFA3IgGA" and "LFA3IgG72A" are preparations of LFA3TIP differing in purity, i.e., 75% and 50%, respectively. hIgG is nonspecific human IgG. "PI-LFA3" is multimeric PI-linked LFA-3. "CD4-IgG" is a fusion protein consisting of a portion of the CD4 protein fused to a portion of the Fc region of IgG. "Mock" refers to a "mock preparation" purified from COS7 cells transfected with an expression vector pSAB132 lacking the DNA sequence encoding LFA3TIP.

Figure 17 depicts results of a PBL proliferation assay as measured by incorporation of ^{3}H-thymidine. PBL proliferation was measured in the presence of LFA3TIP (closed squares), human IgG (closed circles) and a "mock preparation" containing the contaminant ("contamination") which co-purifies with the LFA3TIP used in this assay (closed triangles).

Figure 18 depicts results of an OKT3 (anti-CD3 MAb) dependent PBL proliferation assay as measured by incorporation of ^{3}H-thymidine. PBL proliferation was measured in the presence of 3 nM OKT3 (OKT3), 3 nM OKT3 plus 1 nM or 10 nM LFA3TIP (OKT3 + LFA3TIP), 3 nM OKT3 plus 1 nM or 10 nM human IgG1 (OKT3 + hIgG1), or medium with no OKT3 present (medium).

Figure 19 depicts results of a phytohemagglutinin (PHA) dependent PBL proliferation assay as measured at a suboptimal stimulatory concentration (0.1 μg/ml) and at an optimal stimulatory concentration (1 μg/ml) of PHA. PBL proliferation was measured as indicated in the presence of PHA alone (PHA) and in the presence of PHA plus: PI-linked LFA-3 (+PILFA-3); monomeric soluble LFA-3 (+mon LFA-3); LFA3TIP (+LFA3TIP); an LFA-3-IgG fusion protein which lacks the 10 amino acid M57 region of LFA-3 involved in CD2 binding (+M57IgG); anti-LFA-3 1E6 MAb (+1E6); anti-

CD2 TS2/18 MAb (+TS2/18); and a full-length LFA-3-Ig fusion protein (+FLIgG). Each of the added molecules was present at 5 μg/ml.

DETAILED DESCRIPTION OF THE INVENTION

The polypeptides, compositions, and methods of the present invention are characterized by polypeptides having the amino acid sequence: X_1-X_2-(SEQ ID NO:1)
Asn Arg Val Tyr Leu Asp Thr Val Ser Gly-Y, wherein:

X_1 is hydrogen or methionyl;

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy-terminal 1 to 77 amino acids of the sequence (SEQ ID NO:5): Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino-terminal 1 to 32 amino acids of the sequence (SEQ ID NO:33): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val;

and analogs and derivatives thereof,

said polypeptides being capable of binding to CD2.

In another embodiment, the polypeptides of this invention have the amino acid sequence: X_1-X_2-(SEQ ID NO:1) Asn Arg Val Tyr Leu Asp Thr Val Ser Gly-Y, wherein:

X_1 is hydrogen or methionyl;

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy-terminal 1 to 50 amino acids of the sequence (SEQ ID NO:2): Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino-terminal 1 to 10 amino acids of the sequence (SEQ ID NO:3): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser;

and analogs and derivatives thereof, said polypeptides being capable of binding to CD2.

Preferably, the polypeptides of this invention have the amino acid sequence of amino acids 29-120 of SEQ ID NO:10, amino acids 29-108 of SEQ ID NO:10, amino acids 48-108 of SEQ ID NO:10, and SEQ ID NO:7.

Throughout this specification and in the claims, the abbreviations employed for amino acids and their residues are used in conformity with the generally accepted rules of nomenclature and relate to α-amino acids and their residues of the L-series.

A derivatized amino acid is a natural or non-natural amino acid in which the normally occurring side chain or end group is modified by chemical reaction. Such modifications include, for example, gamma-carboxylation, β-hydroxylation, sulfation, sulfonation, phosphorylation, amidization, esterification, t-butoxy carbonylation, N-acetylation, carbobenzoxylation, tosylation, benzylation, and other modifications known in the art.

A derivatized polypeptide is a polypeptide containing one or more derivatized amino acids.

Analogs of the polypeptides of this invention may be characterized, for example, by amino acid substitutions, additions or deletions, or utilization of D-amino acids. The preferred substitutions in the polypeptides of this invention are those that are recognized in the art to be conservative amino acid substitutions. For example, amino acids belonging to one of the following groups represent conservative changes: ala, pro, gly, glu, asp, gln, asn, ser, thr; cys, ser, tyr, thr; val, ile, leu, met, ala, phe; lys, arg, his; and phe, tyr, trp, his. See, e.g., Grantham, Science, 185, pp. 862-64 (1974); Dayhoff, In Atlas of Protein Sequence and Structure, 5, 1978; Argos, EMBO J., 8, pp. 779-785 (1989).

It should be understood that all analogues and derivatives of this invention are characterized by biological activities that are similar to those of the CD2-binding polypeptides described herein. Accordingly, these analogs and derivatives may be employed in compositions, combinations and methods for diagnosis, therapy and prophylaxis in the same manner as the polypeptides of this invention.

The production of the polypeptides of this invention may be achieved by a variety of methods known in the art. For example, the polypeptides may be derived from the intact transmembrane or PI-linked LFA-3 molecules by proteolysis using specific endopeptidases in combination with exopeptidases, Edman degradation, or both. The intact LFA-3 molecules, in turn, may be purified from natural sources using conventional methods. Alternatively, full-length LFA-3 or truncated forms of LFA-3 may be produced by known

recombinant DNA techniques using cDNAs. (See, United States patent 4,956,281 to Wallner et al.)

Preferably, the polypeptides of the present invention are produced directly, thus eliminating the need for a larger LFA-3 as a starting material. This may be achieved by conventional chemical peptide synthesis techniques or by well-known recombinant DNA techniques, wherein only those DNA sequences which encode the desired polypeptides are expressed in transformed hosts.

A gene which encodes the desired LFA-3 polypeptide of this invention may be designed based on the amino acid sequence of the desired polypeptide. Standard methods may be then applied to synthesize the gene. For example, the amino acid sequence may be used to construct a back-translated gene. A DNA oligomer containing a nucleotide sequence capable of coding for an LFA-3 polypeptide of this invention may be synthesized in a single step. Alternatively, several smaller oligonucleotides coding for portions of the desired polypeptide may be synthesized and then ligated together. Preferably, the DNA sequence encoding an LFA-3 polypeptide of this invention will be synthesized as several separate oligonucleotides which are subsequently linked together. The individual oligonucleotides typically contain 5' or 3' overhangs for complementary assembly.

Once assembled, preferred genes will be characterized by sequences that are recognized by restriction endonucleases (including unique restriction sites for direct assembly into a cloning or an expression vector), preferred codons taking into consideration the host expression system to be used, and a sequence which, when transcribed, produces a stable, efficiently translated RNA. Proper assembly

may be confirmed by nucleotide sequencing, restriction mapping, and expression of a biologically active polypeptide in a suitable host.

One embodiment of a DNA sequence according to this invention comprises the nucleic acid sequence encoding amino acids 1 through 70 of mature LFA-3, i.e., nucleotides 94 through 303 in Figure 1. Another preferred embodiment comprises the nucleic acid sequence (SEQ ID NO:6): AATAGGGTTT ATTTAGACAC TGTGTCAGGT, which codes for amino acids 51-60 of mature LFA-3. However, the preferred DNA sequences of this invention encode polypeptides having the amino acid sequences of amino acids 29-120 of SEQ ID NO:10, amino acids 29-108 of SEQ ID NO:10, amino acids 48-108 of SEQ ID NO:10, and SEQ ID NO:7. The most preferred DNA sequence of this invention encodes a polypeptide having the amino acid sequence 1-120 of SEQ ID NO:10. This sequence when employed in animal cells allows production, secretion and maturation of a polypeptide having the amino acid sequence of amino acids 29-120 of SEQ ID NO:10.

It will be appreciated by those of skill in the art that, due to the degeneracy of the genetic code, DNA molecules comprising many other nucleotide sequences will also be capable of encoding the polypeptides of this invention. These degenerate sequences are encompassed by the present invention.

The present invention also relates to recombinant DNA molecules comprising the aforementioned DNA sequences. The recombinant DNA molecules of this invention are capable of directing expression of the LFA-3 polypeptides of this invention in hosts transformed therewith. A DNA sequence encoding an LFA-3 polypeptide of this invention must be operatively linked to an expression control sequence for such

expression. The term "operatively linked" as used herein refers to positioning in a vector such that transcription and translation of the coding sequence is directed by the control sequence.

To construct a recombinant DNA molecule capable of directing expression of the LFA-3 polypeptides of this invention, the DNA sequences encoding these polypeptides may be inserted into and expressed using a wide variety of vectors. Furthermore, within each specific expression vector, various sites may be selected for insertion of these DNA sequences. These sites are usually designated by the restriction endonuclease which cuts them. They are well recognized by those of skill in the art. It will be appreciated, however, that an expression vector useful in this invention need not have a restriction endonuclease site for insertion of the chosen DNA fragment. Instead, the vector may be joined to the fragment by alternative means.

The expression vector, and in particular the site chosen for insertion of a selected DNA fragment and operative linking to an expression control sequence, is determined by a variety of factors. These factors include, e.g., the number of sites susceptible to a particular restriction enzyme, the size of the polypeptide to be expressed, susceptibility of the desired polypeptide to proteolytic degradation by host cell enzymes, contamination or binding of the polypeptide to be expressed by host cell proteins difficult to remove during purification, expression characteristics, such as the location of start and stop codons relative to the vector sequences, and other factors recognized by those skilled in the art. The choice of a vector and an insertion site for a DNA sequence is determined by a balance of these factors

and not all selections will be equally effective for a given case.

Useful expression vectors for eukaryotic hosts include, for example, vectors comprising expression control sequences from SV40, bovine papilloma virus, adenovirus and cytomegalovirus, and vectors useful specifically in insect cells, such as pVL 941. Useful bacterial expression vectors include known bacterial plasmids, e.g., plasmids from E.coli including colE1, pCR1, pBR322, pMB9 and their derivatives; wider host range plasmids, such as RP4; the numerous derivatives of phage lambda, e.g., NM 989 and the lambda gt series; other DNA phages, e.g., M13 and other filamentous single-stranded DNA phages; and commercially available high expression vectors, e.g., the pGEM series and the lambda Zap vectors. Useful mammalian cell expression vectors include, for example, pNUT. Vectors useful in yeasts include, for example, the 2μ plasmid and derivatives thereof.

Such expression vectors are also characterized by at least one expression control sequence that may be operatively linked to the DNA sequences of this invention inserted in the vector in order to control and to regulate the expression of that cloned DNA sequence. Examples of useful expression control sequences include the malE system, the OmpA system, the lac system, the trp system, the tac system, the trc system, major operator and promoter regions of phage lambda, the control region of fd coat protein, the glycolytic promoters of yeast, e.g., the yeast acid phosphatase, e.g., Pho5, the promoters of the yeast mating factors, and promoters derived from polyoma, adenovirus, retrovirus, and simian virus, e.g., the early and late promoters of SV40, eukaryotic cell promoters, such as the metallothionein promoter and

other sequences known to control the expression of genes of prokaryotic or eukaryotic cells and their viruses or combinations thereof.

The recombinant DNA molecules of the present invention may also comprise other DNA coding sequences fused to and in frame with the DNA sequences of this invention. For example, such constructs may be characterized by an ATG start codon fused directly to the nucleotides encoding the first amino acid of the LFA-3 polypeptide. This construction may produce an f-Met polypeptide. However, it will be understood that the initial methionine may be cleaved during expression in a transformed host or may be subsequently removed. Alternatively, a DNA sequence encoding a bacterial or eukaryotic signal sequence may be fused to the 5' end of a DNA sequence encoding an LFA-3 polypeptide of this invention. This would allow the expressed product to be either secreted or targeted to a specific subcellular compartment within the host cell. Most signal sequences are removed by the host cell after performing their targeting function, thus obviating the need for removal after purification of the desired polypeptide. Many signal sequences, as well as the DNA sequences encoding them, are known in the art. The fusion protein of such signal sequence DNA to and in frame with the sequence encoding an LFA-3 polypeptide of this invention can be achieved by standard molecular biology techniques.

Alternatively, a DNA sequence encoding an LFA-3 polypeptide of this invention may be expressed as a fusion protein by in-frame ligation to a second DNA sequence encoding a host cell polypeptide. The expression of a fusion protein may afford several advantages, such as increased resistance to host cell degradation, ease of identification based upon the

activity or antigenicity of the host cell polypeptide, and ease of purification, based upon the physical or immunological properties of the host cell polypeptide.

This invention also relates to hosts transformed with the recombinant DNA molecules described above. Useful hosts which may be transformed with these recombinant DNA molecules and which may be employed to express the LFA-3 polypeptides of this invention may include well known eukaryotic and prokaryotic hosts, such as strains of E.coli, e.g., E.coli SG-936, E.coli HB 101, E.coli W3110, E.coli X1776, E.coli X2282, E.coli DH1, E.coli DH5-alpha, E.coli MRC1; strains of Pseudomonas; strains of Bacillus, such as Bacillus subtilis; strains of Streptomyces; strains of Saccharomyces; animal cells, such as COS cells, CHO cells, BHK cells, human tissue cells; insect cells (e.g., Spodoptera frugiperda (SF9)); and plant cells in tissue culture. The preferred host for polypeptides claimed herein is CHO cells.

It will be appreciated that not all host/expression vector combinations will function with equal efficiency in expressing DNA sequences encoding the LFA-3 polypeptides of this invention. However, a particular selection of a host-expression vector combination may be made by those of skill in the art after due consideration of the principles set forth herein without departing from the scope of this invention. For example, the selection should be based on a balancing of a number of factors. These factors include, for example, compatibility of the host and vector, toxicity of the polypeptides encoded by the DNA sequence to the host, vector copy number and the ability to control that copy number, the expression of other proteins encoded by the vector, such as

antibiotic markers, ease of recovery of the desired protein, expression characteristics of the DNA sequences and the expression control sequences operatively linked to them, biosafety, costs and the folding, form or any other necessary post-expression modifications of the desired polypeptide.

While recombinant DNA techniques are the preferred method of producing the polypeptides of this invention having a sequence of more than 20 amino acids, shorter polypeptides encompassed by this invention having less than about 20 amino acids are preferably produced by conventional chemical synthesis techniques. Synthetically produced polypeptides of this invention can advantageously be obtained in extremely high yields and be easily purified.

In a preferred embodiment of this invention, the polypeptides are synthesized by solution phase or solid phase polypeptide synthesis and, optionally, digested with carboxypeptidase (to remove C-terminal amino acids) or degraded by manual Edman degradation (to remove N-terminal amino acids). Proper folding of the polypeptides may be achieved under oxidative conditions which favor disulfide bridge formation, as described by S.B.H. Kent, "Chemical synthesis of polypeptides and proteins", Ann. Rev. Biochem., 57, pp. 957-89 (1988). Polypeptides produced in this way may then be purified by separation techniques widely known in the art, preferably utilizing reverse phase HPLC. The use of solution phase synthesis advantageously allows for the direct addition of certain derivatized amino acids to the growing polypeptide chain, such as the O-sulfate ester of tyrosine. This obviates the need for a subsequent derivatization step to modify any residue of the polypeptides of this invention.

The biological activity of the polypeptides of this invention, i.e., their ability to block LFA-3/CD2 interaction, may be assayed using a simple cell binding assay that permits visual (under magnification) evaluation of the binding of LFA-3 polypeptide-expressing cells to CD2-expressing cells. Jurkat cells are preferred as the $CD2^+$ substrate (see Examples, infra.). The binding characteristics of soluble polypeptides according to the invention may be assayed in several known ways, such as by radiolabeling the polypeptide with, e.g., ^{35}S, and then contacting the labeled polypeptide with $CD2^+$ cells. Enzymatic labels or rosetting assays such as described by Seed et al. (Proc. Natl. Acad. Sci. USA, 84, pp. 3365-69 (1987)) may also be used.

In another embodiment of this invention, fusion proteins and DNA sequences coding for them are provided. These fusion proteins have an amino-terminal region characterized by the amino acid sequence of a CD2-binding polypeptide of this invention and a carboxy-terminal region comprising a domain of a protein or polypeptide other than LFA-3. Such domains include, for example, the Fc region of an immunoglobulin.

In the preferred fusion proteins of this invention, the CD2-binding polypeptides of this invention are fused to at least a portion of the Fc region of an immunoglobulin. In these fusion proteins, the CD2-binding polypeptides form the amino-terminal portion, and the Fc region forms the carboxy terminal portion.

In these fusion proteins, the Fc region is preferably limited to the hinge region and the C_H2 and C_H3 domains. More preferably, the Fc region in the fusion proteins of this invention is limited to a

portion of the hinge region, the portion being capable of forming intermolecular disulfide bridges, and the C_H2 and C_H3 domains. See, e.g., Figure 12.

An example of a useful LFA-3-Ig fusion protein of this invention is LFA3TIP (also referred to as LFA-3(92)IgG), which is secreted into the cell culture medium by COS7 cells containing the expression plasmid pSAB152 (see infra). LFA3TIP consists of the amino terminal 92 amino acids of the mature form of LFA-3 fused to a portion of the hinge region and the C_H2 and C_H3 constant domains of human IgG1 (see Figure 11). The fusion protein, LFA3TIP, contains a functional CD2-binding domain of LFA-3 and a sufficient portion of the Fc region of IgG to be recognized by the Fc binding protein, Protein A. LFA3TIP is able to bind to CD2 and inhibit T-cell activation.

It will be apparent that the polypeptides and fusion proteins of this invention may be used in methods to selectively isolate CD2 or CD2-expressing cells, based on the formation of a complex between the CD2-binding domain of those polypeptides and CD2.

In another embodiment of this invention, the polypeptides and fusion proteins of this invention, such as the LFA-3-Ig fusion proteins, may be used to label cells expressing CD2 or a polypeptide containing the LFA-3 binding domain of CD2. For example, the polypeptides and fusion proteins of this invention may be conjugated to a "reporter molecule" which allows detection of the polypeptides or fusion proteins bound to $CD2^+$ cells or polypeptides containing the CD2-binding domain of LFA-3. Owing to the presence of a portion of the immunoglobulin Fc region in the illustrative fusion proteins of this invention, such fusion proteins can be conjugated to the same "reporter molecules" which are commonly conjugated or bound to

immunoglobulins in order to detect immunoglobulins bound to antigens, e.g., ^{125}I, enzyme-conjugated secondary antibodies directed to the Fc region, or biotin-streptavidin based enzyme conjugated molecules. Accordingly an LFA-3-Ig fusion protein of this invention may be conjugated or bound to such reporter molecules via its Fc carboxy-terminal portion. Furthermore, such reporter molecules may be conjugated or bound to the polypeptides or fusion proteins of this invention before or after the polypeptides or fusion proteins have bound to CD2 or to the LFA-3 binding domain of CD2.

It is a further embodiment of this invention that the polypeptides and fusion proteins of this invention can also be used in diagnostic applications to detect the presence or indicate the absence of CD2 or cells or molecules containing the LFA-3-binding domain of CD2.

The polypeptides and fusion proteins of this invention can also be used in therapeutic compositions to inhibit formation of the CD2/LFA-3 complex, when such formation contributes to a pathological state. Alternatively, they may be used therapeutically to mimic the role of LFA-3 in initiating one or more of the T-lymphocyte functional responses dependent on the formation of the CD2/LFA-3 complex (see, e.g., Dustin et al., J. Exp. Med., 165, pp. 677-92 (1987); Springer et al., Ann. Rev. Immunol., 5, pp. 223-52 (1987)). For example, the polypeptides and fusion proteins of this invention may be used in the treatment of acute and chronic inflammation, autoimmune diseases, and for immunomodulation, including treatment of such diseases as systemic lupus erythematosus or lupus vulgaris, rheumatoid arthritis and thyroiditis. Furthermore, the polypeptides and fusion proteins of this invention may

be used to inhibit T-cell activation or to inhibit proliferation of peripheral blood lymphocytes.

In these respects, it is recognized that molecules involved in cell-cell adhesion are generally more effective in eliciting a particular response from a cell when the molecules are present in a multimeric form as opposed to a monomeric form of the same protein. Multimeric forms of cell surface adhesion proteins appear to more closely mimic the typical situation in vivo where, e.g., an effector cell will exhibit hundreds or thousands of copies of a particular adhesion protein on its surface which then bind to the many copies of its ligand on a target cell. When many surface molecules become involved in binding, they may act synergistically, so that the affinity of one cell for another is greater than the mere sum of the binding affinities of the individual molecules. Accordingly, an important aspect of this invention concerns the preparation and use of multimeric forms of the CD2-binding polypeptides disclosed herein.

A variety of methods are known in the art to form multimeric forms of protein monomers. Such methods include using crosslinking agents, e.g., glutaraldehyde (e.g., Reichlin, Methods Enzymol., 70, pp. 159-65 (1980)). If thiol residues are present on a polypeptide or polypeptides, such groups may be oxidized to form intermolecular disulfide bonds to achieve multimeric forms of the polypeptide or polypeptides. Thiol residues or thiol-reactive groups may be introduced into a polypeptide using iminothiolane or heterobifunctional cross-linkers, such as N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), which contains an amine-reactive group and a thiol-reactive group. Coupling of the proteins may then be accomplished through disulfide bonds formed either

directly or through homobifunctional cross-linking agents (see, e.g., Srinivasachar et al., Biochem., 28, pp. 2501-09 (1989); Ramakrishnan et al., Cancer Res., 44, pp. 201-08 (1984); Lambert et al., J. Biol. Chem., 260, pp. 12035-41 (1985)). The effectiveness of disulfide bond formation between molecules would of course be limited to the number of thiols available on the polypeptide (naturally occurring or introduced by derivatization as above) and whether such disulfide bond formation adversely affected the affinity of the resulting multimeric form.

If polypeptides or proteins possess carbohydrate groups, such as in glycoproteins, the sugar moieties of such groups may be used in reactions to link one molecule with another (e.g., Liao et al., J. Biol. Chem., 248, pp. 8247-53 (1973); Moroney et al., Biochem., 26, pp. 8390-98 (1987)).

Other multimeric forms of the CD2-binding polypeptides of this invention may be produced by attaching a phosphatidylinositol ("PI") linkage sequence, e.g., as described in PCT patent application PCT/US90/01859, or sequences of C4 binding protein, e.g., as described in PCT patent application PCT/US91/00567. The hydrophobic PI anchor may be used to form micelles exhibiting a plurality of active CD2-binding domains or multimeric forms of the PI-linked LFA-3, in which a plurality of monomers are associated with one another by hydrophobic interactions between the PI linkage sequences of each monomer (in the absence of added lipids or membrane). In this latter case, multimeric PI-linked LFA-3 molecules are usually octamers; though other polymeric forms have been observed (e.g., 6-12 associated monomers). Alternatively, attaching a segment of DNA encoding the PI linkage sequence downstream of a DNA insert encoding

a polypeptide of the invention, and transfecting suitable mammalian host cells with this construct, will provide a culture of cells exhibiting numerous copies of the CD2-binding polypeptide on their surfaces (attached by a PI anchor).

Alternatively, multiple copies of monomers of polypeptides and fusion proteins of this invention may be bound to another molecule or substrate or particle. As in the case of the binding of LF08 to Affigel-10 beads (see infra), the formation and use of molecules, compounds or particles comprising multiple CD2-binding domains are within the scope of this invention.

In addition, this invention also includes multimeric forms of LFA-3-Ig fusion proteins. Such multimers may be generated by using those Fc regions, or portions thereof, of Ig molecules which are usually multivalent, e.g., IgM pentamers and IgA dimers. It is of course understood that a J chain polypeptide may be necessary to form and stabilize IgM pentamers and IgA dimers. Alternatively, multimers of LFA-3-Ig fusion proteins may be formed by using a protein with an affinity to the Fc region of Ig molecules, such as Protein A. For example, a plurality of LFA-3-Ig fusion proteins, such as LFA3TIP, may be bound to Protein A-agarose beads to form agarose beads whose surfaces are covered with multiple functional CD2-binding domains of the attached LFA-3-Ig fusion proteins.

In another embodiment, this invention provides multimeric proteins capable of binding to CD2, which comprise (a) two or more of the CD2-binding polypeptides described herein, (b) two or more of the CD2-binding fusion proteins described herein, or (c) one or more of the CD2-binding polypeptides and one or more of the CD2-binding fusion proteins.

The polypeptides of this invention may also be used to design low molecular weight (i.e., usually monomeric molecular weights of less than 1000 daltons) nonpeptidyl or only partial peptidyl CD2-binding molecules useful to inhibit cell-cell adhesion via formation of the CD2/LFA-3 complex. Based on the polypeptides provided herein, such small molecules may be designed which possess the ability to bind CD2 and may consist of moieties other than amino acids and may be produced entirely through synthetic methods. The use of such small molecules as therapeutic or diagnostic agents also falls within the scope of this invention.

Another embodiment of this invention involves the use of the CD2-binding polypeptides and fusion proteins to obtain antibodies recognizing the CD2-binding domain of LFA-3. Both monoclonal antibodies (MAbs) and polyclonal antibodies highly specific to the CD2-binding domain of LFA-3 may be obtained utilizing the polypeptides and fusion proteins of this invention.

Methods for obtaining monoclonal antibodies and polyclonal antiserum to a particular antigen are well known in the art. For producing MAbs, an immortal cell line (typically a myeloma cell line) is fused to lymphocytes (typically splenocytes) from a mammal (e.g., a rabbit) immunized with a particular antigen, i.e., in this case the CD2-binding domain of LFA-3. Such fusions usually generate hybridomas, i.e., immortal clones of hybrid cells which produce antibody molecules specific for a single epitope of the immunizing antigen (see, generally, Kohler et al., Nature, 256, pp. 495-97 (1975)). Effective immunization may require that the polypeptide comprising the CD2-binding domain be polymerized or derivatized and mixed with an adjuvant.

It is also necessary to be able to screen the potentially numerous clones of hybridomas generated from the fusions in order to identify those clones which produce antibodies to the CD2-binding domain of LFA-3. For example, such screens may involve assaying the supernatants of cultures of hybridomas for the ability to inhibit CD2-expressing cells from binding to LFA-3 expressing cells. Assays which have been used to screen hybridomas for the production of MAbs to LFA-3 are applicable as primary screens for hybridomas producing MAbs specific for the CD2-binding domain of LFA-3 (see, e.g., Sanchez-Madrid et al., Proc. Natl. Acad. Sci. USA, 79, pp. 7489-93 (1982)).

The DNA encoding the CD2-binding polypeptides of this invention and of deletion mutant forms of the LFA-3 gene, such as those described herein, may also be used as plus/minus probes to detect and isolate other DNA sequences encoding the CD2-binding domain of LFA-3.

The deletion mutant forms of the LFA-3 protein, which lack at least amino acids +51 to +60 of mature LFA-3; at least amino acids +41 to +50 of mature LFA-3 or at least amino acids +31 to +40 of mature LFA-3; (and preferably lack all 3 regions) may be used to clear polyclonal antiserum of antibodies which recognize epitopes of LFA-3 other than the epitopes within the CD2-binding domain of LFA-3. Such mutants may be, for example, selected from the group consisting of M57, M55, M56, PIM3 and M100, and combinations thereof. For example, a polyclonal anti-LFA-3 antiserum may be preincubated with a mutant form of the LFA-3 protein encoded by the mutant LFA-3 gene containing the M57 or M100 deletion mutations (Figure 1 and Figure 6). The polyclonal antibodies recognize and bind LFA-3 epitopes on the mutant LFA-3 protein. However, since the CD2-binding domain is not present,

antibodies to this epitope in the polyclonal antiserum will not bind. Precipitation of the complexes that do form will result in an enrichment for any antibodies remaining in the antiserum that are specific for epitopes of the CD2-binding domain.

The CD2-binding domain polypeptides and fusion proteins of this invention may be formulated as pharmaceutical compositions using conventional methods to prepare pharmaceutically useful compositions and combinations. Such compositions preferably include at least one pharmaceutically acceptable carrier. See, e.g., Remington's Pharmaceutical Sciences, (E.W. Martin). Pharmaceutical compositions of the present invention typically contain, in addition to the active polypeptide, a pharmaceutically acceptable buffer, preferably phosphate buffered saline, together with a pharmaceutically acceptable compound for adjusting isotonic pressure, such as sodium chloride, mannitol or sorbitol. The pharmaceutically acceptable compositions and methods of this invention are characterized by pharmaceutically effective amounts of a polypeptide according to the invention.

The pharmaceutical compositions and combinations of this invention which comprise LFA-3-Ig fusion proteins may be used, for example, to inhibit the activation of T-lymphocytes or to inhibit the proliferation of peripheral blood lymphocytes (see infra).

The term "combination" as used herein, includes a single dosage form containing at least one polypeptide of this invention and at least one other pharmaceutically active agent, a multiple dosage form wherein the polypeptide and the other active agent are administered separately, but concurrently, or a multiple dosage form wherein the two components are

administered separately but sequentially. Alternatively, the polypeptides of this invention and the other active agent may be in the form of a single conjugated molecule. Conjugation of the two components may be achieved by standard cross-linking techniques well known in the art. A single molecule may also take the form of a recombinant fusion protein.

The pharmaceutical compositions and combinations of this invention may be administered to a patient in any pharmaceutically acceptable dosage form, including, but not limited to, those which may be administered to a patient intravenously as a bolus or by continued infusion, intramuscularly, subcutaneously, intracutaneously, intra-articularly, orally or parenterally.

Methods for determining pharmaceutically effective dosages are known to those skilled in the art. The dosage and dose rate will depend on a variety of factors such as the specific composition, the object of the treatment, i.e., therapy or prophylaxis, method of administration, and the judgment of the treating physician.

This invention also relates to the bioanalytic use of CD2-binding polypeptides and fusion proteins, or compositions containing them, for determining the concentration of CD2 proteins or the detection of CD2-expressing cells in a biological sample. These polypeptides and compositions may be used in a manner similar to that of reagents employed in conventional assays. In addition, the polypeptides of this invention may be utilized in diagnostic kits designed to detect the presence and measure the concentration of CD2 or CD2-expressing cells.

In order that this invention may be better understood, the following examples are set forth.

These examples are for purposes of illustration only, and are not to be construed as limiting the scope of this invention.

EXAMPLE 1

Preparation of Deletion Mutations In the LFA-3 Gene

In order to map the CD2-binding domain on the LFA-3 protein, a series of deletion mutations of the LFA-3 gene were systematically generated using site-specific mutagenesis by oligonucleotide heteroduplexing. cDNA encoding transmembrane has been isolated and sequenced (see, Wallner et al., United States Patent 4,956,281), and a bacteriophage bearing cDNA coding for transmembrane LFA-3 was deposited with American Type Culture Collection in Rockville, Maryland (accession number 75107). A plasmid, pHT16-6, containing cDNA encoding transmembrane LFA-3 was obtained from Biogen, Inc. (Cambridge, Massachusetts) and used in preparing all the deletion mutations. The construction of plasmid pHT16-6 is described in PCT patent publication WO 88/09820, which is herein incorporated by reference. Plasmid pHT16-6 contains a cDNA insert encoding LFA-3 and contains a unique EcoRI site near the 5' end of the LFA-3 coding sequence, a unique BamHI site adjacent the 5' end of the LFA-3 cDNA, a unique HindIII site adjacent the 3' end of the LFA-3 cDNA, two NotI sites 1112 bp apart and bracketing the LFA-3 cDNA, and a unique ScaI site. The cDNA insert of pHT16-6 containing the entire coding region for transmembrane LFA-3 is shown in Figure 1.

In this procedure, seventeen sequences of the LFA-3 coding sequence, each 30 bp long, were selected for deletion. For each proposed deletion, a 30-base antisense oligonucleotide (30-mer) was synthesized which consisted of the complementary 15 bases

immediately upstream of (5' to) the proposed deletion and the complementary 15 bases immediately downstream of (3' to) the proposed deletion. Hybridization of a particular synthetic oligonucleotide to a strand of the LFA-3 DNA resulted in a heteroduplex in which a specific sequence of 30 bp would loop out. By this mutagenesis procedure, some of the replication products of the heteroduplex contained deletion mutations lacking the 30 bp region looped out by heteroduplex formation.

The synthetic oligonucleotides used to generate the seventeen deletion mutants depicted in Figure 1 are set forth in the following table:

Sequence	Complementary to LFA-3 Nucleotides	Segment Deleted
SEQ ID NO:13	109-123+154-168	M53
SEQ ID NO:14	139-153+184-198	M54
SEQ ID NO:15	169-183+214-228	M55
SEQ ID NO:16	199-213+244-258	M56
SEQ ID NO:17	229-243+274-288	M57
SEQ ID NO:18	259-273+304-318	M58
SEQ ID NO:19	289-303+334-348	M59
SEQ ID NO:20	319-333+364-378	M60
SEQ ID NO:21	349-363+394-408	M61
SEQ ID NO:22	379-393+424-438	M62
SEQ ID NO:23	409-423+454-468	M63
SEQ ID NO:24	439-453+484-498	M64
SEQ ID NO:25	469-483+514-528	M65
SEQ ID NO:26	499-513+544-558	M66
SEQ ID NO:27	529-543+574-588	M90

SEQ ID NO:28	559-573+604-618	M91
SEQ ID NO:29	589-603+634-648	M92.

For each heteroduplex, one sample of plasmid pHT16-6 (100 μg) was digested with HindIII (210 units, New England Biolabs) and either EcoRI (300 units, New England Biolabs) or BamHI (300 units, New England Biolabs). Another sample of pHT16-6 (100 μg) was linearized by digestion with ScaI (300 units, New England Biolabs). Digestion products were electrophoresed on 1 percent (w/v) agarose gels in TAE buffer (40 mM Tris/acetate, 1 mM EDTA, pH 8.0), and the desired fragment from each digestion was then electroeluted from the gel (Maniatis et al., Molecular Cloning: A Laboratory Manual (Cold Spring Harbor, 1982)). In the case of the ScaI digestion, the linearized pHT16-6 was electroeluted from the gel; in the case of the HindIII/EcoRI or HindIII/BamHI digestions of pHT16-6, the larger of two restriction fragments produced in each case was electroeluted.

A sample of the ScaI linearized pHT16-6 DNA (100 ng) was mixed with a sample of the isolated HindIII/EcoRI or HindIII/BamHI restriction fragment (100 ng) and with 8 picomoles of one of the seventeen antisense oligonucleotides previously phosphorylated with ATP (Maniatis et al., supra). Referring to Figure 1, since the EcoRI restriction site is located in the M56 region, the HindIII/EcoRI large restriction fragment could not be used to generate deletions of regions M53, M54, M55 and M56. Thus, the HindIII/BamHI large restriction fragment was used in the procedure to generate these four deletions.

In order to form heteroduplexes, a synthetic oligonucleotide, ScaI-linearized pHT16-6, and either HindIII/EcoRI or HindIII/BamHI large fragment of

pHT16-6 were mixed in 100 mM NaCl, 80 mM $MgCl_2$, 6.5 mM Tris/Cl, pH 7.6 and boiled for 3 minutes to denature. The denatured DNA was allowed to anneal at 37°C for 1 hour, then at 4°C for 1 hour, and finally at 0°C for 10 minutes.

After annealing, the gaps in the heteroduplexes were filled in and the fragments ligated in a single reaction mixture by adding to the annealed DNA the following constituents to give the indicated final concentrations or amounts: ATP (20 mM); dATP, dTTP, dGTP, dCTP (each at 10 mM); Klenow (large fragment of DNA Polymerase I, 2.5 units, New England Biolabs); T4 DNA ligase (200 units, New England Biolabs). The mixtures were then incubated overnight at 15°C.

After incubation, half of each fill-in/ligation mix was used to transform 100 µl of E.coli JA221 (Maniatis et al., supra). Colonies of transformed cells were selected on LB plates supplemented with ampicillin (50 µg/ml) (Maniatis et al., supra).

Colonies of transformants were screened for the presence of a particular deletion by colony hybridization using the particular oligonucleotide used in the heteroduplex to generate the deletion as a probe.

For use as probes, a sample of each oligonucleotide (80 pmol) was labeled using ^{32}p-ATP by standard procedures. The labeled oligonucleotides were precipitated with 2 M ammonium acetate (Maniatis et al., supra). Labeled probe was added to the hybridization buffer at a final activity of approximately 5 x 10^5 CPM/ml of hybridization mixture. Hybridizations were carried out on nitrocellulose filters at 60°C for about 8 hours. After washing the

filters in 0.5 x SSC buffer at 60°C, autoradiography was performed and positive colonies scored (Maniatis et al., supra). The generation of the desired deletion mutations was confirmed by DNA sequence analysis (Maxam and Gilbert, in Methods in Enzymology (Grossman and Moldave, eds.), 65, pp. 499-560 (1980)) of plasmid DNA in colonies scoring positive according to hybridization results.

These procedures produced plasmids, each containing one of the 30 bp deleted sequences listed above and depicted in Figure 1. The plasmid containing the M57 deletion in the LFA-3 coding sequence was designated plasmid pLFA3M57-4A.

EXAMPLE 2

Construction of Recombinant Expression Plasmids

Plasmids prepared according to Example 1 with successfully deleted 30 bp segments from the LFA-3 coding sequence were used for construction of expression vectors. Aliquots of 100 μg of plasmids having deleted segments (see Figure 1) M54, M55, M56, M57, M58, M63 and M65, respectively, were digested with NotI endonuclease (100 units, New England Biolabs, Beverly, Massachusetts). For M57, M63 and M65, the 5' overhangs were filled in using a standard Klenow (New England Biolabs) reaction mix (Maniatis et al., supra) to generate blunt ended restriction fragments. The fragments were purified from 0.7% TAE agarose gels by electroelution.

The gel-purified, blunt-ended, NotI fragments were then individually cloned into the SmaI site of the eukaryotic expression vector pBG368PY (Dailey et al., J. Virol., 54, pp. 739-49 (1985)) using T4 ligase at 15°C overnight. NotI fragments of M54, M55, M56, and M58 were gel purified as described above and ligated to

NotI-digest expression vector, PMDR902. The resulting ligations were used to transform E.coli JA221 and positive colonies of transformants containing the recombinant plasmids carrying the desired inserts were identified by colony hybridization, as described above. The orientation of the M57, M63 and M65 inserts in the vector was confirmed by EcoRI digestion, generating 6600, 4000 and 200 bp fragments for correctly oriented inserts, which were separated on 0.7% agarose gel. For plasmids containing M54, M55, M56 and M58 inserts, the orientation was determined by PvuII digestion analysis, where the correct orientation generated fragments of 6599 bp, 1185 bp and 506 bp. All fragments were verified by DNA sequencing (Maxam and Gilbert, supra).

The recombinant expression plasmids carrying DNA encoding the M54, M55, M56, and M58 LFA-3 deletion mutations were linearized with AatII and electroporated into Chinese Hamster Ovary (CHO) cells according to the published protocol of J. Barsoum (DNA Cell Biol., 9, pp. 293-300 (1990)). Plasmids carrying DNA encoding the M57, M63 and M65 deletion mutations were linearized using NruI and electroporated into CHO cells as above, except that 19 μg of the NruI-digested DNA was ethanol precipitated overnight at -20°C with 1 μg of EcoRI-digested SV2 DNA ($DHFR^+$) and 380 μg of sonically disrupted salmon sperm DNA. CHO cells (1×10^7) were electroporated with the coprecipitated DNA at 280 volts using a BioRad Gene Pulser.

After electroporation, cells were seeded into two 100 mm plates in $alpha^+$ MEM, 10% fetal calf serum (FCS), 4 mM L-glutamine, penicillin/streptomycin, then incubated for 48 hours at 37°C. The cells in the plates were then divided into five 100 mm plates containing $alpha^-$ MEM, 10% FCS, 4 mM L-glutamine, penicillin/streptomycin, and incubated for five days at

37°C. The cells were then fed with alpha⁻ Complete Medium supplemented with 200 nM methotrexate for M57, M63 and M65, and 50 nM methotrexate for M54, M55, M56 and M58. Each plate was grown to 90% confluency then assayed by FACS (Fluorescence-Activated Cell Sorter) to determine whether any of the CHO cultures transfected with the LFA-3 deletion mutations expressed the mutant forms of LFA-3.

EXAMPLE 3

FACS Analysis of Transfected Cells

Transfected CHO cells, prepared in Example 2 and grown in the presence of methotrexate to 90% confluency, were rinsed twice with HANKS BSS medium (Ca^{++} and Mg^{++} free, pH 7.0) and removed with HANKS (Ca^{++} and Mg^{++} free, 5 mM EDTA, pH 7.0) medium. Approximately 2 x 10^5 cells were resuspended in 100 µl of a solution of cold (0°C) wash buffer (PBS, 0.1% NaN_3, 0.5% bovine serum albumin (BSA), pH 7.2), and a primary antibody was added. The primary antibody was either anti-LFA-3 MAb TS2/9 ascites fluid (see, e.g., Sanchez-Madrid et al., Proc. Natl. Acad. Sci. USA, 79, pp. 7489-93 (1982), obtained from Dana Farber Cancer Inst., Boston, Massachusetts); the anti-LFA-3 MAb 7A6 (obtained from Biogen, Inc., Cambridge, MA; 1.6 µg/ml); or anti-LFA-3 polyclonal rabbit antiserum 202 (obtained from Biogen, Inc.). All the primary antibodies are known to block CD2 adhesion to LFA-3. The amount of primary antibody used was typically between 1 and 2 µl. Cells were incubated at 0°C for 45 minutes and washed twice with wash buffer.

A fluorescein-labeled secondary antibody was then added and the mixture incubated for 30 minutes at 0°C. For analysis with the monoclonal antibodies, the

secondary antibody was fluorescein (DTAF)-conjugated affinity purified goat anti-mouse $F(ab)_2$ IgG (H+L) (Jackson Immunoresearch Laboratories, Inc., West Grove, CA); for use with the polyclonal rabbit antiserum 202, the secondary antibody was fluorescein isothiocyanate (FITC) goat anti-rabbit IgG (H+L) (Fisher Biotech, Pittsburgh, Pennsylvania).

After incubation with the secondary antibody, cells were overlayed with 300 µl FCS, washed twice in wash buffer, resuspended in 300 µl 1 x PBS and transferred to Falcon 2052 tubes to be read on the cell sorter.

Referring to Figure 2, the FACS analyses indicated that cells transfected with expression vectors containing deletion mutations M57 (Figures 2A and 2B), M65 (Figures 2C and 2D), M63 (Figures 2E and 2F), M54 (Figures 2G and 2H), M55 (Figures 2I and 2J), M56 (Figures 2K and 2L), and M58 (Figures 2M and 2N) expressed a surface protein that was recognized by the anti-LFA-3 polyclonal antiserum 202 (Figures 2A, 2C, 2E, 2G, 2I, 2K, 2M). However, the anti-LFA-3 MAbs TS2/9 and 7A6 bound only to transfectants carrying the M65 and M63 deletion mutants and not to transfectants lacking the M57, M54, M55, M56, or M58 regions (compare Figures 2B, 2H, 2J, 2L, 2N with 2D, 2F). These results indicated that the M54, M55, M56, M57 and M58 segments, which were deleted from the LFA-3 protein in, respectively, the deletion mutations M54, M55, M56, M57 and M58 (see Figure 1), were important in CD2 recognition of the LFA-3 molecule.

EXAMPLE 4

Jurkat Cell Binding Assay

CHO cells transfected with the M57 deletion mutation ("M57/CHO" cells), CHO cells transfected with plasmid p24 (see, Wallner et al., PCT patent application WO 90/02181) expressing PI-linked LFA-3 ("P24/CHO" cells, positive control), and normal CHO cells (negative control) were tested for the ability to bind Jurkat cells expressing CD2.

M57/CHO cells, P24/CHO cells and CHO cells (1×10^5) were added to separate wells of a 6-well plate (Corning) and washed twice with RPMI Complete Medium. Jurkat cells ($CD2^+$), obtained as a gift from Dr. Timothy Springer (Dana Farber Cancer Inst., Boston, Massachusetts) were washed three times with a solution of RPMI, 10% FCS, 4 mM L-glutamine, and then 5×10^6 cells were added to each well and incubated for 4 hours at 0°C. Cells were then washed gently three times with RPMI and examined under the microscope at 40X and 100X magnification for cell-cell binding.

Referring to Figure 3, whereas positive control cells expressing PI-linked LFA-3 bound Jurkat cells expressing CD2 (Figure 3C), M57/CHO cells failed to bind Jurkat cells (Figure 3B), as did nontransfected ($LFA\text{-}3^-$) CHO cells (Figure 3A).

EXAMPLE 5

Northern Blot Analysis of mRNA from M57/CHO Cells

The mRNA of M57/CHO cells was analyzed by Northern blot as a further confirmation that the failure of the monoclonal antibodies, i.e., MAbs TS2/9 and 7A6, to bind to the M57/CHO cells was due to the surface LFA-3 mutant lacking the M57 CD2-binding region

rather than to inefficient expression of the mutant LFA-3 gene.

RNA from about 1 x 10^7 M57/CHO cells on a 100 mm plate was isolated as follows: Growth media were removed and 2 ml extraction buffer (50 mM Tris-Cl (pH 7.5), 1% SDS, 5 mM EDTA, proteinase K added to 100 µg/ml immediately prior to use) was added. The plate was incubated 20 minutes at 37°C with gentle shaking. A viscous cell lysate developed and was collected in a 50 ml test tube. An equal volume of phenol:chloroform:ether (50:50:1) was added and the mixture vortexed briefly. The mixture was homogenized on a Polytron mixer (Kinematica, Switzerland) for 15 seconds at highest speed to shear the DNA. The mixture was poured into a 15 ml Corex tube and centrifuged at 10,000 rpm, 10 minutes at 4°C.

After centrifuging, the aqueous phase was collected and NaCl was added to 0.25 M, followed by 1 volume of isopropanol. This mixture was placed on dry ice for 10 minutes, defrosted and centrifuged 15 minutes at 10,000 rpm and 4°C.

The pellet was resuspended in 2.9 ml distilled water and vortexed. 0.9 ml of 12 M LiCl was added (to 2.8 M) and the suspension allowed to stand at least four hours at 4°C. 5S RNA and DNA remained in solution; other RNA fractions precipitated. This solution was centrifuged for at least 15 minutes at 10,000 rpm at 4°C.

The pellet was resuspended in 360 µl distilled water and transferred to an Eppendorf tube. 40 µl 3 M NaAc (pH 5.2) and 1 ml ethanol were added, then the mixture was cooled at -70°C for 5 minutes, cooled at -20°C for 15 minutes, centrifuged, rinsed with ethanol, and resuspended in 400 µl 0.3 M NaAc. Ethanol (1 ml) was added and the precipitation was

repeated. The RNA recovered after centrifuging was resuspended 100 µl distilled water.

10 µg of the RNA were electrophoresed on a 1% agarose-formaldehyde gel, transferred to a GeneScreen nitrocellulose membrane (New England Nuclear) and hybridized to a ^{32}P-labeled probe. As a control, RNA extracted from the cell line M16.3/CHO (expressing recombinant soluble LFA-3, obtained from Biogen, Inc., Cambridge, Massachusetts) was analyzed on the same Northern blot. The Northern blot analysis (Figure 4) indicated efficient synthesis of the M57 RNA in the M57/CHO cells.

EXAMPLE 6

Immunoprecipitation of LFA-3 Deletion Mutant

To verify the loss of specific antibody binding domains in the mutant LFA-3 expressed on the surface of M57/CHO cells, M57/CHO transfectants, untransfected CHO cells, and P24/CHO transfectants (which express PI-linked LFA-3) were surface labeled with ^{125}I, and each of the three primary antibody preparations (i.e., polyclonal antiserum 202, MAb TS2/9 and MAb 7A6) were used to immunoprecipitate LFA-3 after detergent disruption of the surface membrane.

About 10^7 (each) of M57/CHO cells, normal CHO cells and P24/CHO cells suspended in $PBS^=$ (i.e., PBS without Ca^{++} and Mg^{++}) supplemented with 5 mM EDTA were washed three times with $PBS^=$ and resuspended in 0.5 ml PBS. Washed cells were added to glass tubes (12 x 75 mm^2) previously coated with a solution of 50 µg 1,3,4,6-tetrachloro-3α,6α-diphenylglycoluril (Iodo-Gen, Pierce Bio-Research, Rockford, Illinois) in 100 µl $CHCl_3$ and dried in nitrogen. Just before use, the tubes were rinsed with PBS, and then ^{125}Iodine (1 mCi)

was added and the tubes incubated on ice for 30 minutes, with swirling every 10 minutes.

After incubation, the iodinated cells were added to 10 ml alpha⁻ MEM, 10% FCS, 4 mM L-glutamine. The cells were spun down, washed twice with 5 ml of the same medium, and then resuspended in 1 ml PBS and centrifuged again. The washed cells were then lysed by resuspension in 1 ml DOC buffer (20 mM Tris/Cl, pH 7.3; 50 mM NaCl, 0.5% deoxycholate (DOC); 0.5% NP40) containing 20 µl of protease inhibitor PMSF (Sigma Chemical Co., St. Louis, Missouri, 17 mg/ml in ethanol), followed by incubation for 30 minutes on ice. The lysate was then microcentrifuged for 10 minutes at 4°C, and the supernatants containing the ^{125}I-labeled surface molecules removed.

Lysates from the foregoing iodinations were precleared by contacting with 50 µl of protein A-Sepharose and incubating on a rocker for 1 hour at room temperature. 100 µl of lysate was removed for each sample and mixed with 300 µl of DOC buffer. This mixture was centrifuged and the resulting cleared supernatant removed to a new tube.

Primary antibody was added to samples of each of the cleared supernatants: Polyclonal anti-LFA-3 antiserum 202 was used at a final concentration 40 µg/ml; MAbs TS2/9, 7A6 and a control monoclonal antibody, MOPC-21 (IgG1, not specific to LFA-3) were used at 5 µg/ml. 100 µl DOC and 2 µl protease inhibitor PMSF were added, and the mixtures incubated on a rocker for 2 hours at room temperature 25°C or overnight at 4°C.

After incubation, 30 µl of protein A-Sepharose (for polyclonal antiserum 202 samples) or 15 µl of anti-mouse IgG-agarose (Sigma Chemical Co.) (for MAb samples) was added to the samples, followed by

incubation on a rocker for 2 hours at room temperature. The mixtures were then centrifuged for 2 minutes, and the supernatants carefully removed and discarded. 1 ml of DOC buffer was then added, and the pellets resuspended by vortexing. The resuspended material was then washed 3 times with DOC buffer.

To prepare the samples for analysis by polyacrylamide gel electrophoresis, 30 µl of SDS sample buffer was added, the sample heated at 65°C for 15 minutes. The sample was then centrifuged for 2 minutes, and the supernatant removed and saved for electrophoresis. 15 µl of the supernatant was run on a denaturing 10-20% gradient polyacrylamide gel (Daiichi system, Enprotech), and autoradiography performed to identify immunoprecipitated surface proteins.

Figure 5 is an autoradiograph of an SDS polyacrylamide gel showing antibody-precipitated LFA-3 surface proteins from M57/CHO, normal CHO, and P24/CHO cells. This gel revealed that TS2/9, 7A6 and the polyclonal antiserum 202 precipitated LFA-3 from the CHO cells expressing the PI-linked LFA-3 (lanes 9, 10, 11). In contrast, only polyclonal antiserum 202 precipitated the LFA-3 surface protein from M57/CHO cells expressing the deletion mutant M57 LFA-3 gene (lane 4).

EXAMPLES 7 and 8

The 10-amino acid region removed in the M57 deletion mutant (see Figure 1) is adjacent to but does not contain a N-linked glycosylation site. To investigate whether the region of the M57 deletion is involved directly in CD2-binding or indirectly disrupts CD2-binding by causing a conformational change in the CD2-binding domain of LFA-3, two additional experiments were performed.

First, three large deletion mutants were generated, each of which lacked a span of 59 amino acids compared to the native LFA-3 molecule. The regions deleted are shown by underlining in Figure 6 and were designated M100, M101 and M102. The object of this experiment was to determine whether the conformational changes inherent in the large M101 and M102 deletions would alter recognition of the M57 region (see Figure 1) and to demonstrate that the entire CD2 binding domain was encompassed in the M100 region.

Second, a synthetic oligopeptide, LF08, having the amino acid sequence (SEQ ID NO:7) Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr (amino acids +50-+65 of mature LFA-3 (see Figure 1)) was isolated and fixed to a solid substrate, then used in a Jurkat cell rosetting assay to determine if CD2-expressing cells would recognize the isolated M57 region of LFA-3 (see Figure 1).

Preparation of Large Deletion Mutants

Figure 6 depicts the amino acid sequence and nucleotide sequence of transmembrane LFA-3 and shows with underlining the three regions, designated M100, M101 and M102, which were deleted from LFA-3 cDNA to yield genes capable of directing the expression of three large deletion mutants.

Following the procedure used in Example 1, a 30-base antisense oligonucleotide was synthesized which consisted of sequences complementary to the 15 bases of the sense strand upstream of (5' to) and to the 15 bases downstream of (3' to) the desired deletion region. The synthetic oligonucleotides used to generate the large deletion mutations are shown below:

	Sequence	Complementary to LFA-3 Nucleotides	Segment Deleted
	SEQ ID NO:30	109-123+304-318	M100
	SEQ ID NO:31	289-303+484-498	M101
	SEQ ID NO:32	469-483+634-648	M102.

Heteroduplexing was carried out as described in Example 1, except that 200 ng of LFA-3 cDNA was used. Colony hybridizations were carried out using 1 x 10^6 CPM/ml ^{32}P-ATP kinased oligonucleotides at 65°C and washed with 0.5x SSC at 60°C. Positives were screened by EcoRI digestion and isolation of 2900 bp and 500 bp fragments on a 0.7% TAE agarose gel.

Construction of expression vectors was performed by excising the LFA-3 cDNA from deletion mutation plasmids prepared above with NotI. Aliquots of 50 μg of a eukaryotic expression plasmid PMDR902 (obtained from Biogen, Inc., Cambridge, Massachusetts) were digested with 50 units of NotI, and the isolated NotI fragments (0.06 pmol), containing the deletion mutations M100, M101 and M102, were ligated to 0.02 pmol PMDR902 DNA, and the ligated products were used to transform E.coli JA221.

Positive clones were screened by colony hybridization using oligonucleotides 18, 19 and 20, having the sequences of SEQ ID NO:30, SEQ ID NO:31 and SEQ ID NO:32, respectively, as probes. The orientation of the inserts was determined by PvuII restriction analysis, which generated bands of approximately 6599, 1737 and 500 bp on 20.7% TAE agarose gel for correctly oriented constructs. The sequence was confirmed by DNA sequencing as described above. The resulting recombinant expression plasmids containing the M100, M101 and M102 deletion mutations were designated

pPMDRM100-4, pPMDRM101-1 and pPMDRM102-8, respectively. The resulting expression plasmids were electroporated into CHO cells as in Example 2, except the cells were split into medium containing 25 nM and 50 nM methotrexate.

The M100/CHO, M101/CHO and M102/CHO transfectants were subjected to a Jurkat cell binding assay, as described in Example 4 above. The results are shown in Figure 7. M101/CHO cells (Figure 7C) and M102/CHO cells (Figure 7D), which express a surface protein having the intact M57 CD2-binding region of LFA-3, showed clumping characteristic of Jurkat/CHO cell binding. CHO control cells (Figure 7A) and M100/CHO cells (Figure 7B) showed no such clumping, indicating the absence of a surface structure on the CHO cell surface recognized by Jurkat cells.

Jurkat Binding to Immobilized LF08 Peptide

1.4 mg of the synthetic peptide LF08 (SEQ ID NO:7) or control hepatitis B peptide MXC-01 (SEQ ID NO:4) at 2 mg/ml in deionized water was coupled to 100 µl agarose gel beads (Affi-Gel 10, BioRad, Richmond, California) according to the following protocol: 100 µl of Affi-Gel 10 slurry was transferred to a small Buchner funnel and the solvent drained. The beads were washed with three bed volumes of cold (4°C) deionized water, transferred to 700 µl of the LF08 solution, and then incubated for 4 hours at 4°C on a rocker. A spectrum taken of the supernatant, before and after coupling of LF08, indicated that a coupling efficiency of 80% had been achieved.

After coupling, unreacted coupling sites were blocked by incubating the LF08 beads or MXC-01 beads with ethanolamine/HCl (93 mM, pH 7.9) overnight at 4°C with gentle shaking. The blocked beads were then

washed three times with PBS supplemented with 0.5 M NaCl and three times with PBS supplemented with 10% FCS.

Jurkat cells (2 x 10^5) were washed twice with RPMI, 4 mM L-glutamine, 10% PBS and combined with 2.5 or 15 µl of LF08/Affi-Gel 10 beads or MXC-01/Affi-Gel 10 beads to a final volume of 20 µl. The mixture was incubated for 30 or 60 minutes at room temperature. After incubation, the cells were transferred to 200 µl RPMI in a 96-well flat bottom plate (Corning), and observed under a microscope at 40X and 100X. Figures 8A and 8B show characteristic results of contacting the LF08/Affigel beads with Jurkat cells, resulting in binding of coated beads to the surface of Jurkat cells. Figure 8C shows characteristic results of the MXC-01/Affigel beads failing to bind to the surface of Jurkat cells.

EXAMPLES 9 and 10

A further deletion mutant was prepared which provided a PI-linked surface polypeptide on CHO cells having the N-terminal 89 amino acids of native LFA-3. Referring to Figure 9, the nucleotides deleted from cDNA encoding PI-linked LFA-3 are shown by the underlined region, PIM3. The PIM3 nucleotides were deleted using the same heteroduplex deletion mutagenesis strategy described above (Example 1). In this case, a 30-base antisense oligonucleotide (oligonucleotide 320.03), having the 5'-3' sequence (SEQ ID NO:8) TAATGGATTG CTAAGAAAGA ACTTCATGGT, was used for deletion mutagenesis.

Plasmid p24 (100 ng), containing the cDNA encoding PI-linked LFA-3 was digested with NotI, and the large restriction fragment (lacking the PI-linked LFA-3 coding sequence) was isolated. Additional p24

DNA was linearized with ScaI. The large NotI restriction fragment and the ScaI-linearized DNA were denatured, mixed with oligonucleotide 320.03, and allowed to reanneal as described in Example 1. After annealing, the gaps in the heteroduplexes were filled in, and the fragments ligated as described in Example 1.

The filled-in, ligated heteroduplexes were then transformed into E.coli JA221 and the transformants screened by colony hybridization using a ^{32}P-labeled 320.03 oligonucleotide (1 x 10^6 cpm/ml) at 60°C as described above. The hybridization filters were washed in 0.5X SSC at 65°C and positive colonies identified by autoradiography. Plasmid DNA was isolated from each of the positive colonies, and digested with NotI. Digestion of one of the plasmids, pPIM3-6, with NotI yielded fragments of 2648 and 640 bp, confirming that pPIM3-6 contained the desired PIM3 deletion in the PI-linked LFA-3 coding sequence.

The 640 bp NotI fragment of pPIM3-6 was cloned into the NotI site of the expression vector PMDR902 (a gift of Dr. M.D. Rosa, Biogen, Inc., Cambridge, Massachusetts), and used to transform E.coli JA221 cells. Transformants were screened by colony hybridization using the ^{32}P-labeled 320.03 oligonucleotide as probe. Plasmids from positive colonies were then isolated, and the orientation of the DNA insert determined by restriction enzyme analysis using PvuII. Recombinant plasmid pPMDRM3-10 contained PvuII fragments of 6399, 1634 and 495 bp, indicating that this plasmid contained the mutated PI-linked LFA-3 gene in the proper orientation for expression in the PMDR902 vector.

Expression of PIM3 Deletion Mutant

pPMDRM3-10 was electroporated into CHO DHFR$^-$ cells and amplified with 25 and 50 nM methotrexate as described above. Cells from plates containing confluent growth were assayed by FACS using MAbs TS2/9 and 7A6 as described above. The PIM3 deletion mutant form of LFA-3 expressed in a cell line designated PIM3.25.2 exhibited epitopes involved with CD2/LFA-3 complex formation.

To determine whether the protein recognized by TS2/9 and 7A6 on PIM3.25.2 cells was PI-linked, the protein expressed on the surface of PIM3.25.2 cells was tested for its susceptibility to release by treatment with phosphatidylinositol-specific phospholipase C (PI-PLC, obtained from Biogen, Inc.). Cells of PIM3.25.2 were grown to 70 percent confluency in two 100 mm culture plates and removed with PBS supplemented with EDTA (5 mM) as described above. One-third of these cells was treated with PI-PLC (1 μl; Biogen, Inc.) at 37°C for 45 minutes in 100 μl of alpha$^-$ MEM supplemented with 10% FCS, L-glutamine (2 mM), pen-strep mix (1X), and 25 nM methotrexate. The cells were then centrifuged for 15 seconds in an Eppendorf microcentrifuge and washed two times in FACS buffer (PBS, 0.5% BSA, 0.1% sodium azide, pH 7.2). The washed cells were then resuspended in FACS buffer containing FITC-labeled goat anti-mouse IgG (1:50 dilution from serum). The cells were then washed twice with FACS buffer, resuspended in 300 μl of PBS and transferred to Falcon 2052 tubes for FACS analysis.

Referring to Figure 10, cells of PIM3.25.2 clearly express a protein on their cell surface that is recognized by TS2/9 (Figure 10A, dashed line) and is also susceptible to release from the cell surface by PI-PLC treatment (Figure 10A, dotted line). Since the

PIM3 protein expressed in cells of clone PIM3.25.2 possesses LFA-3 epitopes recognized by MAb TS2/9, which blocks CD2/LFA-3 complex formation, it was concluded that the 89 amino acid N-terminal region of the mature LFA-3 molecule contains the conformational requirements necessary for CD2/LFA-3 complex formation.

To increase expression of the PIM3 mutant LFA-3 protein, the PIM3.25.2 clone was amplified in alpha$^-$ MEM supplemented with 10% FCS in 50, 100 and 200 nM of methotrexate. Cells were plated in 96-well microtiter plates at a concentration of 20 cells/ml, grown to confluency (12-17 days) and expanded to 100 mm plates for subsequent FACS analysis as described for PIM3.25.2, except that expression of the PIM3 mutant form of LFA-3 was monitored using the 7A6 MAb (Figure 10B, dashed line). The results of the FACS analysis indicated that the amplified cell line, PIM3.25.2.100.12, expressed approximately ten-fold higher amounts of the PIM3 mutant form of PI-linked LFA-3. Treatment of the PIM3.25.2.100.12 cells with PI-PLC released about 80% of the PIM3 mutant LFA-3 (Figure 10B, dotted line).

EXAMPLE 11

Construction of plasmid pSAB144

pSAB144 contains the human IgG1 constant region sequences excluding the C_H1 region and the first cysteine of the amino terminal portion of the hinge region. The human IgG1 heavy chain constant region was isolated from a partial Sau3A human fibroblast genomic library (EMBL/5X, a gift of Dr. Mark Pasek). The library DNA was cleaved with HindIII and PvuII. DNA fragments corresponding to approximately 3 kb were ligated to the vector fragment of pSP65 (Promega, Madison, Wisconsin) generated by cleavage of pSP65

using HindIII and HincII. The resulting plasmid was designated pAB1. Plasmid pAB1 was used as a source of DNA encoding the IgG1 heavy chain constant region.

In order to isolate a cDNA copy of the IgG1 heavy chain region, RNA was prepared from COS7 cells which had been transiently tranfected by the plasmid VCAM1-IgG1 (also known as pSAB133). Construction of plasmid VCAM1-IgG1 is described in PCT patent application WO 90/13300. The RNA was reverse transcribed to generate cDNA using reverse transcriptase and random hexamers as the primers. After 30 min. at 42°C, the reverse transcriptase reaction was terminated by incubation of the reaction at 95°C for 5 min. The cDNA was then amplified by PCR (Polymerase Chain Reaction, see, e.g., Sambrook et al., Molecular Cloning, Vol. 3, pp. 14.1-14.35 (Cold Spring Harbor; 1989)) using the following kinased primers:

370-31:

(SEQ ID NO:34): 5'TCGTC GAC AAA ACT CAC ACA TGC C,
(SEQ ID NO:35) asp lys thr his thr cys

which contains a SalI site, and

370-32 (SEQ ID NO:36):

5' GTAAATGAGT GCGGCGGCCG CCAA,

which encodes the carboxy terminal lysine of the IgG1 heavy chain constant region, followed by a NotI site.

The PCR amplified cDNA was purified by agarose gel electrophoresis and glass bead elution for cloning in plasmid pNN03. Plasmid pNN03 was constructed by removing the synthetic polylinker sequence from the commercially available plasmid pUC8 (Pharmacia, Piscataway, New Jersey) by restriction endonuclease digestion and replacing the synthetic polylinker sequence with the following novel synthetic sequence (SEQ ID NO:37):

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG

ATCTGCAGCA TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC.

The purified PCR amplified cDNA fragment was ligated to pNN03 which had been cleaved with EcoRV, dephosphorylated, and purified by low melt agarose gel electrophoresis. The ligation reaction was used to transform E.coli JA221 and the resulting colonies were screened for a plasmid containing an insert of approximately 700 bp. The identity of the correct insert was confirmed by DNA sequence analysis, and the plasmid was designated pSAB144.

Construction of Plasmid pSAB149

The plasmid pSAB149 was constructed as follows. The LFA3-encoding plasmid pHT16-6 was subjected to PCR amplification using oligonucleotides 320-04 and 320-05. Oligonucleotide 320-04 includes a NotI site and the nucleotides corresponding to amino acids 1 through 7 of the LFA-3 signal sequence:

(SEQ ID NO:38) 5' GAGGCGGCCG CC ATG GTT GCT GGG AGC GAC GCG,

(SEQ ID NO:39) met val ala gly ser asp ala.

Oligonucleotide 320-05 corresponds to the LFA-3 amino acids 86-92 and includes a SalI site (SEQ ID NO:40): 5' AAGTCGACAT AAAGAAAGAA CTTCAT. The amplified DNA fragment was ligated to the vector fragment of pNN03, cleaved by EcoRV.

Construction of pSAB132

pJOD-S (Barsoum, J., DNA and Cell Biol., 9, pp. 293-300 (1990)) was modified to insert a unique NotI site downstream from the adenovirus major late promoter so that NotI fragments could be inserted into the expression vector. pJOD-S was linearized by NotI cleavage of the plasmid DNA. The protruding 5' termini

were blunt-ended using Mung Bean nuclease, and the linearized DNA fragment was purified by low melting temperature agarose gel electrophoresis. The DNA fragment was religated using T4 DNA ligase. The ligated molecules were then transformed into E.coli JA221. Colonies were screened for the absence of a NotI site. The resulting vector was designated pJOD-S delta Not1. pJOD-8 delta Not1 was linearized using SalI and the 5' termini were dephosphorylated using calf alkaline phosphatase. The linearized DNA fragment was purified by low melting temperature agarose gel electrophoresis and ligated in the presence of phosphorylated oligonucleotide ACE175, which has the following sequence: (SEQ ID NO:41) TCGACGCGGC CGCG. The ligation mixture was transformed into E.coli JA221, and colonies were screened for the presence of a plasmid having a NotI site. The desired plasmid was named pMDR901.

In order to delete the two SV40 enhancer repeats in the SV40 promoter which controls transcription of the DHFR cDNA, pMDR901 and pJODΔe-tPA (Barsoum, DNA and Cell Biol., 9, pp. 293-300 (1990)) were both cleaved with AatII and DraIII. The 2578 bp AatII-DraIII fragment from pMDR901 and the 5424 bp AatII-DraIII fragment from pJODΔe-tPA were isolated by low melting temperature agarose gel electrophoresis and ligated together. Following transformation into E.coli JA221, the resulting plasmid, pMDR902, was isolated. pSAB132 was then formed by eliminating the EcoRI-NotI fragment of pMDR902 containing the adenovirus major late promoter and replacing it with an 839 bp EcoRI-NotI fragment from plasmid pCMV-B (Clontech, Palo Alto, California) containing the human cytomegalovirus immediate early promoter and enhancer.

Construction of pSAB152

pSAB144 was cleaved with SalI and NotI, and the 693 bp fragment isolated. pSAB149 was cleaved with SalI and NotI and the 365 bp fragment was isolated. The two fragments were ligated to pSAB132, which had been cleaved with NotI, and the 5' termini dephosphorylated by calf alkaline phosphatase. The resulting plasmid, pSAB152, contained the DNA sequence encoding the LFA-3 signal sequence, the amino terminal 92 amino acids of mature LFA-3, ten amino acids of the hinge region of IgG1 and the C_H2 and C_H3 constant domains of IgG1 (see Figure 12). E.coli JA221 transformed with pSAB152 is deposited with American Type Culture Collection, Rockville, Maryland (accession no. 68720).

Construction of pNNM57-14

As mentioned in Example 1, plasmid pLFA3M57-4A contains a DNA sequence encoding LFA-3 with a deletion of the 30 bp M57 region (i.e., nucleotides 244-273 of SEQ ID NO:9). This coding sequence of pLFA3M57-4A was subjected to PCR amplification using oligonucleotide 320-04 (SEQ ID NO:38) and oligonucleotide 320-05 (SEQ ID NO:40) in order to amplify the DNA encoding the signal sequence and the first 82 amino acids of the M57 deletion mutant of LFA-3. The PCR amplified DNA was purified by low melting temperature agarose gel electrophoresis.

The purified, PCR amplified DNA was then ligated into the EcoRV site of plasmid pNNO3. The ligated DNA was transformed into E.coli JA221, and the resulting transformants screened (by NotI digestion) for a plasmid containing an approximately 300 bp insert. The identity of the desired insert was confirmed by DNA sequence analysis. The desired

plasmid containing the approximately 300 bp insert was designated pNNM57-14.

Construction of pM57Ig-5

Plasmid pNNM57-14 was cleaved with NotI and SalI, and the 310 bp fragment isolated by low melting temperature agarose gel electrophoresis. This fragment and the 693 bp SalI-NotI fragment of pSAB144 (see supra) were ligated to NotI-digested, calf alkaline phosphatase-treated pSAB132 (see supra). The ligation mixture was used to transform E.coli JA221, and transformant colonies were screened by hybridization using a γ-^{32}P-ATP labeled oligonucleotide having the sequence of SEQ ID NO:17. The desired orientation of the inserts in pSAB132 was confirmed by the identification of a 6913 and a 2029 bp fragment upon digestion with PvuII. The resulting plasmid was designated pM57Ig-5. DNA sequence analysis confirmed that pM57Ig-5 contains a DNA sequence encoding the LFA-3 signal sequence, the first 82 amino acids of the M57 deletion mutant of LFA-3, ten amino acids of the hinge region of human IgG1 and the C_H2 and C_H3 constant domains of IgG1.

EXAMPLE 12

Production of LFA3TIP From Transiently Transfected COS7 Cells

To produce the LFA-3-Ig fusion protein, LFA3TIP (also referred to as LFA-3(92)IgG), plasmid pSAB152 DNA was transfected into COS7 cells by electroporation as follows. Four aliquots of 200 µg each of pSAB152 DNA each were ethanol precipitated with 350 µg of sonicated salmon sperm DNA. DNA was pelleted and resuspended in 0.8 ml of 1 x HEBS (20 mM Hepes/pH 7.05, 137 mM NaCl, 5 mM KCl, 0.7 mM Na_2HPO_4, 6 mM

dextrose). COS7 cells from 4 confluent T150 flasks (8 x 10^7 cells) were removed by trypsin treatment in DMEM (Gibco, Gaithersburg, Maryland), 10% fetal bovine serum, 4 mM glutamine. Cells from each flask were transferred to individual 15 ml Corning polypropylene tubes and pelleted at 1000 rpm for 4 minutes at room temperature in an IEC centrifuge. Medium was aspirated, and cells resuspended in the DNA-HEBS solution and transferred to a Bio-Rad (Richmond, California) electroporation cuvette. The cuvettes were set in a Bio-Rad Gene Pulser and pulsed at 280 volts and 960 μFd capacitance. Cells were resuspended in 10 ml of DMEM medium and pelleted in an IEC centrifuge as described above. All cells were seeded into a 2 liter cell factory in DMEM medium, and culture medium was harvested after 72 hours for purification of LFA3TIP protein.

The concentration of secreted LFA3TIP in transfected COS7 culture medium was determined by ELISA. Fisher 96 flat bottom well plates (Corning 2580) were coated with 50 μl of goat anti-human IgG (H+L) (Jackson Immuno Research, West Grove, Pennsylvania, Catalogue No. 109-005-088) diluted at 5μg/ml in 1X PBS. These plates were incubated at 4°C overnight. Plates were washed the next day 6 times with dH_2O and blocked with 150 μl/well of block buffer (2% normal goat serum in 1X PBS). Buffer was removed after a 2 hour incubation at room temperature and conditioned medium was added at various dilutions. As a control to create a standard curve, a series of dilutions of whole human IgG (Jackson Immuno Research, West Grove, Pennsylvania, Catalogue No. 099-000-603) was included on the same plate. After a one hour incubation at room temperature, plates were washed 4 times with 0.01% Tween 20 in 1X PBS, and 50 μl/well of

a 1:5000 serum dilution of alkaline phosphatase-conjugated anti-human IgG specific for Fc fragment (Jackson Immuno Research, West Grove, Pennsylvania, Catalogue No. 109-055-098) was added to each well. After one hour, plates were washed 6 times with 0.1% Tween 20.

Plates were developed with a solution containing a 1:10 dilution of 10 mM Ca^{2+}, Mg^{2+} in 10% diethanolamine, pH 9.6, plus 5 mg/ml 4-nitrophenylphosphate (Boehringer Mannheim Biochemicals, Indianapolis, Indiana, catalogue no. 738-352). The reaction was stopped using 3N NaOH and plates read at 405 nM on a Microdevices microplate reader.

Production Of LFA3TIP From
A Stably Transformed CHO Cell Line

A recombinant LFA3TIP expression vector was constructed as described below, which can be stably maintained in CHO cells to achieve continuous expression of LFA3TIP.

A NotI fragment containing the LFA3TIP coding sequence of pSAB152 was purified by low melting temperature agarose gel electrophoresis. The fragment was ligated into the NotI cloning site of the expression plasmid pMDR902 (see Example 11). The resulting ligations were used to transform E.coli JA221, and colonies containing the desired, correctly oriented, insert were identified by the presence of 6599, 2058, and 487 bp fragments upon digestion with PvuII. The identity of the correct insert in pMDR902 was confirmed by DNA sequence analysis. The resulting recombinant expression plasmid was designated pMDR(92)Ig-3.

The recombinant expression plasmid pMDR(92)Ig-3 was electroporated into CHO cells according to the published protocol of J. Barsoum (DNA

Cell Biol., 9, pp. 293-300 (1990)), with the following changes. 50 μg of AatII-digested plasmid DNA and 350 μg of sonicated salmon sperm DNA were used in the electroporation protocol. In addition, cells were selected in alpha⁻ complete medium supplemented with 25 or 50 nM methotrexate (MTX).

To determine expression levels of secreted LFA3TIP, clones were transferred to a flat bottom 96 well microtiter plate, grown to confluency and assayed by ELISA (see infra). One clone grown in the presence of 25 nM MTX, LFA3TIP.25.11, expressed 5-10 μg of LFA3TIP per ml of culture medium. This clone was expanded and amplified further. Amplification was carried out by seeding 1 cell per well in a 96 well plate with complete medium supplemented with 50 or 100 nM MTX. Clones were grown to confluency and assayed by ELISA. Two clones, LFA3TIP.25.11.50.10A and LFA3TIP.25.11.50.5B, secreted higher levels (i.e., 50-60 μg of LFA3TIP per ml of culture medium) of LFA3TIP and were expanded for further study and purification.

The concentration of secreted LFA3TIP in medium of cultures of CHO cells carrying pMDR(92)Ig-3 (i.e., conditioned medium) was determined by ELISA.

Wells of Immulon 2 plates (Dynatech, Chantilly, Virginia) were each coated with anti-LFA3 MAb TS2/9 (gift of Dr. Timothy Springer) with 50 μl of anti-LFA3 TS2/9 MAb diluted to 25 μg/ml in 0.05 M sodium carbonate/bicarbonate buffer, pH 9.6, covered with Parafilm, and incubated overnight at room temperature. The next day, plates were washed 6 times with deionized water and blocked with 150 μl/well of a block buffer (5% fetal calf serum in 1X PBS), which had been filtered through a 2 micron filter. The buffer was removed after a 2 hour incubation at room temperature, and conditioned medium was added at

various dilutions. As a control to create a standard curve, a series of dilutions of LFA-3 (50 µl per well) was also included. Typically, the well containing the most concentrated LFA-3 standard contained 50 µl of an LFA-3 solution containing 10 ng of LFA-3 in 1X PBS. Block buffer diluted in 1X PBS constituted the negative control. The samples and controls were incubated at room temperature for one hour.

The plates were then washed 6 times with deionized water. Each well was then filled with 50 µl of a 1:5000 dilution of rabbit polyclonal anti-LFA-3 antiserum (e.g., antiserum 202, supra) in 5% fetal calf serum in 1X PBS. After one hour at room temperature, the polyclonal anti-LFA-3 antiserum was removed and the wells were washed 4 times with a solution of 0.05% Tween-20 in 1X PBS. Each well was then filled with 50 µl of HRP-goat anti-rabbit IgG(H+L) (Jackson Immuno Research Laboratories, Inc., West Grove, Pennsylvania; Catalogue No. 111-035-045) at a 1:10,000 dilution in the block buffer containing 2% whole mouse serum (Cappel, Catalogue No. 5011-1380). The plates were then incubated at room temperature for 50-60 minutes.

The HRP-goat anti-rabbit IgG(H+L) solution was removed, and the wells were washed 6 times with 0.05% Tween-20 in 1X PBS. Then, 50 µl of HRP-substrate buffer was added to each well at room temperature. HRP-substrate buffer was prepared as follows: 0.5 ml of 42 mM 3,3',5,5'-tetramethylbenzidine (TMB), (ICN Immunobiologicals, Lisle, South Carolina, Catalogue No. 980501) in DMSO (Aldrich) was slowly added to 50 ml of substrate buffer (0.1 M sodium acetate/citric acid, pH 4.9); followed by addition of 7.3 µl of 30% hydrogen peroxide (Sigma, Catalogue No. H-1009).

The development of a blue color in each well was monitored at 650 nm on a microtiter plate reader.

After 7-10 minutes, the development was stopped by the addition of 50 µl of 2 N sulfuric acid. The resulting yellow color was read at 450 nm on a microtiter plate reader. A negative control well was used to blank the machine.

Production of M57IgG

A fusion protein consisting of LFA3TIP lacking the ten amino acid M57 region of LFA-3 (M57IgG) was produced substantially as described above for LFA3TIP.

EXAMPLE 13

Purification of LFA3TIP

The COS7(pSAB152) conditioned culture medium was concentrated 10-fold using an AMICON S1Y30 spiral cartridge system (AMICON, Danvers, Massachusetts). The concentrate was divided into 4 x 50 ml aliquots and batch-adsorbed with 200 µl per aliquot of Protein-A Sepharose 4B (SIGMA, St. Louis, Missouri) overnight at 4°C. The beads were pelleted at 1000 rpm in a clinical centrifuge, combined, and then packed into a 5 mm diameter column. The resin was washed with 20 ml of PBS supplemented with 500 mM NaCl followed by 20 ml of PBS. The bound proteins were eluted in 150 µl fractions with 50 mM glycine, 250 mM NaCl (pH 3.0) into tubes containing 15 µl of 1 M HEPES, pH 7.8. 10 µl of each fraction was run on 12% nonreducing SDS-PAGE gels. The fractions containing the eluted protein were pooled and subjected to Superose-12 gel filtration chromatography developed in PBS (Pharmacia/LKB, Piscataway, New Jersey).

Aliquots of 10 µl of the peak protein fractions (determined by measuring the O.D. at 280 nm) were run on 12% SDS-PAGE gels under nonreducing

conditions and the fractions containing LFA3TIP with a low concentration of contaminating proteins, as determined on the SDS-PAGE gels and by Western blot analysis (see, e.g., Towbin et al., Proc. Natl. Acad. Sci. USA, 74, pp. 4350-54 (1979); Antibodies: A Laboratory Manual, pp. 474-510 (Cold Spring Harbor Laboratory, 1988)), were pooled and concentrated in a YM30 Centricon (AMICON, Danvers, Massachusetts). LFA-3 was detected on Western blots using rabbit anti-LFA-3 polyclonal antiserum 202 (see Example 3, supra) and goat anti-rabbit IgG, which was labeled with horseradish peroxidase (Sigma, St. Louis, Missouri). Blots were developed using the Amersham ECL detection kit (RPN 2106, Amersham, Arlington Heights, Illinois). The final pool was run on 12% SDS-PAGE gels under nonreducing conditions to assess the purity. A UV absorbance spectrum was run to determine the concentration. All preparations purified with Protein A were found to contain a single contaminant, which most likely is bovine IgG, present in the fetal calf serum of the culture medium, and which copurifies with the LFA3TIP.

The purity of LFA3TIP was determined by denaturing and nondenaturing SDS-PAGE (Figure 13). The results of the SDS-PAGE analysis indicated that LFA3TIP, purified from the culture medium of COS7 cells carrying plasmid pSAB152, is present in the cell culture medium as a dimer of two monomeric LFA-3-Ig fusion proteins, connected by disulfide bonds.

The fact that LFA3TIP is found in the cell culture medium suggests that, as with LFA-3, the signal peptide sequence operates normally, i.e., the signal peptide is cleaved from the amino terminal region of the LFA-3 domain of LFA3TIP in the process of secreting LFA3TIP protein across the cell membrane.

Purification of M57IgG

M57IgG was purified from conditioned culture medium substantially as described above for LFA3TIP. Similar contaminants were observed.

EXAMPLE 14

FACS Analysis of LFA3TIP Binding

Jurkat cells were transferred into several Eppendorf tubes at 1 x 10^5 cells/tube. Cells were pelleted for 10 seconds in an Eppendorf microcentrifuge, the medium was aspirated off, and pellets were resuspended in 100 µl of LFA3TIP or anti-CD2 monoclonal antibody (MAb) TS2/18 (Sanchez-Madrid et al., Proc. Natl. Acad. Sci. USA, 79, pp. 7489-7493 (1982)), both at 10 µg/ml in FACS buffer (PBS, 0.1% NaN_3, 0.5% BSA pH 7.2). Cells were incubated on ice for 30 minutes, washed twice with FACS buffer, and incubated with 100 µl of the appropriate secondary antibody to detect MAbs bound to the Jurkat cells. FITC conjugated goat anti-mouse IgG (H+L) $F(ab')_2$ (Jackson Immunoresearch) was used to detect the anti-CD2 MAb, TS2/18, and R-Phycoerythrin conjugated AP goat anti-human IgG $F(ab')_2$ (Jackson Immunoresearch) was used to detect LFA3TIP bound to Jurkat cells. The FITC goat anti-mouse IgG $F(ab')_2$ was diluted to a 1:50 concentration in FACS buffer, and the R-Phycoerythrin conjugated AP goat anti-human IgG $F(ab')_2$ was diluted by 1:20 in FACS buffer. Cells were incubated for 30 minutes on ice, washed 2 times and resuspended in 300 µl of 1 x PBS and fluorescence detected on a cell sorter.

For competition studies, Jurkat cells were pelleted in Eppendorf tubes as described above and

LFA3TIP was added at a concentration of 10 μg/ml in FACS buffer. Cells were incubated for 30 minutes on ice and washed twice with FACS buffer. Pellets were then resuspended in 100 μl of a 1:100 dilution (in FACS buffer) of anti-CD2 MAb-containing ascites fluids: $T11_1$, $T11_2$ or $T11_3$ (all were gifts of Dr. Ellis Reinherz, Dana Farber Cancer Institute, Boston, Massachusetts). Cells were incubated for 30 minutes on ice, washed twice and resuspended in a 1:20 dilution of R-phycoerythrin conjugated AP goat anti-human IgG $F(ab')_2$ to detect bound LFA3TIP. After a 30 minute incubation on ice, cells were washed twice and resuspended in 300 μl of 1 x PBS and analyzed in a cell sorter.

The TS2/18 monoclonal antibodies and the monoclonal antibodies in ascites fluid $T11_1$ are specific for the LFA-3 binding domain of CD2. Thus, these antibodies are expected to bind to CD2 molecules on the surface of Jurkat cells and occupy the same site at which LFA3TIP binds. Accordingly, when Jurkat cells were incubated first with an excess of TS2/18 MAb or $T11_1$ ascites fluid, few if any domains are expected to be available for R-Phycoerythrin conjugated LFA3TIP to molecules to bind. As shown in Figure 14A, preincubation of Jurkat cells with either the TS2/18 MAB or $T11_1$ ascites fluid resulted in few cells being labeled with LFA3TIP. A signal nearly identical to unstained control cells was observed. In contrast, in the absence of either TS2/18 or $T11_1$ ascites fluid, LFA3TIP bound to Jurkat cells and labeled a significant proportion of the cells (Figure 14A).

The MAbs present in $T11_2$ and $T11_3$ ascites fluid are specific for CD2, but recognize epitopes distinct from the epitope of CD2 involved in CD2/LFA-3 complex formation. As shown in Figure 14B,

preincubation of Jurkat cells with either $T11_2$ or $T11_3$ ascites fluid did not prevent LFA3TIP from binding to the Jurkat cells. The results shown in Figure 14A and 14B indicate that LFA3TIP possesses the functional CD2-binding domain LFA-3.

EXAMPLE 15

Mixed Lymphocyte Reaction

A functional assay for the formation of the CD2/LFA-3 complex and T-cell activation is the mixed lymphocyte reaction ("MLR") (see, e.g., Krensky et al., J. Immunol., 131(2), pp. 611-616 (1983); Bradley, "Mixed Lymphocyte Responses", in Selected Methods in Cellular Immunology (Mishell and Shiigi, eds.), pp. 162-164 (W.H. Freeman & Co., San Francisco 1980). This assay is based on the activation of T-lymphocytes in a population of peripheral blood lymphocytes ("PBLs") when the T-lymphocytes ("responder cells") recognize alloantigens in nonproliferating allogenic PBLs ("stimulator cells"). Such activation occurs due to cell to cell adhesion, mediated in part by the binding of CD2 molecules on the T-lymphocytes to the LFA-3 molecules on the allogeneic PBLs.

PBLs were purified from 30 ml blood of two allogeneic human donors over a Ficoll-Paque gradient (Pharmacia, Piscataway, New Jersey, catalog no. 17-0840-02). Blood was diluted at a 1:2 ratio in RPMI medium and overlayed on a Ficoll gradient at a 2:1 ratio (30 ml blood:15 ml Ficoll). Cells were centrifuged through the gradient in a Sorvall RT6000 centrifuge at 1600 rpm, 20°C, for 30 minutes. The interface containing PBLs was collected into 50 ml polypropylene centrifuge tubes (Corning 25331) and topped with RPMI medium. The cells were then pelleted by centrifugation in a Sorvall RT6000 centrifuge at

1400 rpm, 4°C, for 15 minutes. The cells of the pellets were washed twice with 50 ml RPMI and pelleted as described above. PBLs were resuspended in RPMI complete medium (RPMI, 10% Hyclone FCS, 4 mM glutamine, Pen-Strep) to a concentration of 3 x 10^6 cells/ml. To produce stimulator cells, PBLs from one of the donors were irradiated at 2000 rads in a Gammacell Irradiator and brought to a final concentration of 3 x 10^6 cells/ml.

Antibodies or LFA3TIP samples were added at the concentrations indicated in Figure 15 to a polystyrene 96 round bottom well plate (Corning 25850). The highest concentration used for both the MAbs and LFA3TIP was 5 μg/ml. All dilutions and incubations were done in RPMI complete medium. Responder cells (nonirradiated) and irradiated stimulator cells were added to wells at a 1:1 ratio at a final concentration of 1.5 x 10^5 cells per well each and plates were incubated for five days at 37°C. On the fifth day, cells were pulsed with 1 μCi [methyl-^{3}H] thymidine (New England Nuclear, Boston, Massachusetts, NET-027) for fifteen hours, and harvested on a Tomtech 96 well harvester. Proliferation of the nonirradiated population of T-lymphocytes was measured by determining incorporation of the ^{3}H-thymidine into the cells, indicating uptake of the labeled thymidine during T-lymphocyte proliferation. Using this MLR assay, a variety of MAbs and CD2-binding molecules were tested for their effect on CD2/LFA-3 complex formation and T-cell activation.

The anti-LFA-3 MAb 1E6 (produced by hybridoma 1E6-2C12, ATCC accession no. HB 10693) is specific for the CD2-binding domain of LFA-3. As shown in Figure 15, when 1E6 MAbs were present in the MLR assay, a dose dependent inhibition of T-cell activation was

observed. This result is consistent with the view that 1E6 MAbs bind the CD2-binding domain of LFA-3, prevent CD2/LFA-3 complexes from forming between stimulator and responder cells, and thereby inhibit activation of T-cells in the responder cell population.

LFA3TIP exhibited a similar dose dependent inhibition of T-cell activation in the MLR assay (see Figure 15). To exclude the possibility that the IgG portion of the 1E6 MAbs or LFA3TIP contributed to the observed inhibition of T-cell activation, non-specific human IgG1 (Pierce, Rockford, IL) was tested in the MLR assay. As shown in Figure 15, the nonspecific human IgG did not exhibit the dose dependent inhibition of T-cell activation seen with LFA3TIP or the 1E6 MAbs.

Taken together, these results demonstrate that the inhibitory activity of LFA3TIP on T-cell activation in the MLR assay resides in the LFA-3 domain and not the IgG domain of the fusion protein.

Inhibitory Activity on T-cell
Activation of Other Molecules

In addition to LFA3TIP and 1E6 MAbs, the following molecules were also tested for inhibitory activity on T-cell activation in the MLR assay: 7A6 MAb (MAb specific for the CD2-binding domain of LFA-3, produced by hybridoma 7A6-2E5, ATCC accession no. HB 10695), TS2/18 (anti-CD2 MAb, Sanchez-Madrid et al., supra), hIgG (nonspecific total human IgG1), PI-LFA3 (multimeric PI-linked LFA-3 formed by intermolecular hydrophobic interaction at the PI anchor region of each PI-LFA-3 monomer), and a CD4-IgG1 fusion protein (analogous to LFA3TIP, but containing an amino terminal region consisting of a portion of CD4, see, e.g., PCT application WO 89/01940).

A comparison of the inhibitory activity of each of these molecules is shown in the bar graph of

Figure 16. "LFA3IgGA" and "LFA3IgG72A" in Figure 16 are preparations of LFA3TIP differing in purity, i.e., 75% and 50% respectively. As a control, a "mock" preparation, purified from COS7 cells transfected with vector DNA alone (i.e., no DNA insert encoding LFA3TIP), was added to show that the inhibitory activity on T-cell activation was not derived from a nonspecific inhibitor contained in conditioned COS7 cell culture medium. The mock preparation contains the contaminant which, as discussed in Example 13, copurifies with LFA3TIP and probably is bovine IgG present in the fetal calf serum of the growth medium. All MLR assays were carried out as described above, except that each preparation of molecules was assayed at a concentration of 0.1 μg protein/ml.

MAbs which recognize the CD2-binding domain of LFA-3 (7A6 and 1E6) or the LFA-3 binding domain of CD2 (TS2/18) exhibited significant inhibitory activity on T-cell activation. The ability of LFA3TIP to inhibit T-cell activation increased with purity (compare LFA3IgG72A, 50% purity, with LFA3IgGA, 75% purity). Nonspecific human IgG1 and the CD4-IgG1 fusion protein failed to inhibit T-cell activation.

The multimeric form of PI-linked LFA-3 also failed to inhibit T-cell activation. Despite the plurality of CD2-binding sites in multimeric PI-linked LFA-3, it appears that this type of multimer neither inhibits nor enhances the human allogeneic MLR.

EXAMPLE 16

PBL Proliferation Assay

Human PBLs were isolated from 20 ml of human donor blood on a Ficoll-Paque gradient, as described above. Purified LFA3TIP was added to 96 well polystyrene round bottom tissue culture plates (Corning

25850) at the concentrations indicated in Figure 17. PBLs (1×10^5) were then added to each well, and plates were incubated for 3 days at 37°C. All dilutions were carried out in RPMI complete medium (see Example 15). Cells were pulsed after 3 days with 1 μCi/well [methyl-^{3}H] thymidine for 15 hours and harvested on a Tomtech 96 well automatic harvester. As controls, PBL proliferation was measured in growth medium alone and in growth medium supplemented with nonspecific human IgG1.

As shown in Figure 17, the LFA3TIP preparation inhibited proliferation of PBLs. Nonspecific human IgG1 did not inhibit PBL proliferation.

We also assayed the major contaminant in the LFA3TIP preparation from a mock preparation as described in Example 15. As mentioned in Examples 13 and 15 above, this contaminant is probably bovine IgG from the growth medium. Figure 17 shows that, as with the nonspecific human IgG1, the contaminant also did not inhibit proliferation of PBLs.

PHA and OKT3 Dependent PBL Proliferation

We next assessed the ability of LFA3TIP to inhibit OKT3 dependent (i.e., anti-CD3 dependent) T-cell proliferation. PBLs were isolated as described above from one healthy human donor. For OKT3 dependent PBL proliferation, aliquots of 1×10^5 donor PBLs were incubated for 2 days with 3 ng/ml of OKT3 (Ortho Pharmaceuticals, Raritan, New Jersey) alone, and in the presence of LFA3TIP (1 nM and 10 nM) or purified human IgG1 (Pierce Chemical Co., Rockford, Illinois) (1 nM and 10 nM). One aliquot of cells was incubated in medium alone, without OKT3. The cells were then pulsed

with [methyl-^{3}H] thymidine as described above. The results of this experiment are shown in Figure 18.

The results in Figure 18 show that LFA3TIP was significantly more effective at inhibiting OKT3 dependent PBL proliferation than the control human IgG1 of irrelevant specificity. As with the results in Figure 17, this indicates that the ability of LFA3TIP to inhibit PBL proliferation resides primarily in the 92 amino acid LFA-3 region, which contains the CD2 binding domain, and not in the IgG portion of LFA3TIP.

We also assessed the ability of LFA3TIP and various other CD2-binding molecules, as well as, the ability of M57IgG, to inhibit phytohemagglutinin (PHA) dependent PBL proliferation, at both suboptimal and optimal concentrations of PHA.

For this assay, 1 x 10^5 donor cells (human PBLs) were incubated with PHA (Fisher) at 0.1 or 1.0 μg/ml, either alone or in the presence of PI-linked LFA-3 ("PILFA-3", Wallner et al., PCT patent application WO 90/02181), monomeric soluble LFA-3 ("mon LFA-3", consisting of amino acids 29-181 of SEQ ID NO:10), LFA3TIP, M57IgG (see Example 11), a full-length soluble LFA-3-IgG fusion protein ("FLIgG", consisting of amino acids 29-181 of SEQ ID NO:10 fused to a portion of the hinge region and the C_H2 and C_H3 domains of human IgG1), an anti-CD2 MAb (TS2/18, gift of T. Springer), or an anti-LFA-3 MAb (1E6) produced by hybridoma 1E6-2C12 (ATCC HB 10693). FLIgG was at a concentration of 2 μg/ml; all the other proteins were at a concentration of 5 μg/ml. The cells were then pulsed with [methyl-^{3}H] thymidine as described above. The results are displayed in Figure 19.

Referring to Figure 19, when PHA was incubated with human PBLs at a suboptimal concentration (i.e., 0.1 μg/ml), only PI-linked LFA-3 (PILFA-3) was

able to stimulate PBL proliferation. M57IgG, monomeric soluble LFA-3 and FLIgG had no effect on suboptimal PHA-stimulated T-cell proliferation. MAb 1E6 and MAb TS2/18 inhibited proliferation 80-90%; LFA3TIP inhibited 70%.

When PHA was present at an optimal level to stimulate PBL proliferation, LFA3TIP, MAb 1E6 and MAb TS2/18 inhibited T-cell proliferation by 41%, 26% and 20%, respectively.

The results in Figure 19 indicate that the region of LFA-3 defined by the N-terminal 92 amino acids, containing the CD2-binding domain of LFA-3, is capable of inhibiting PHA dependent PBL proliferation, but that the absence of a portion of the CD2-binding domain, as in M57IgG, or the presence of additional LFA-3 amino acid sequence, as in PI-linked LFA-3, monomeric LFA-3 or FLIgG, diminishes the ability of the CD2-binding domain of LFA-3 to inhibit PHA dependent PBL proliferation.

Taken together, the results indicated that inhibition of PBL proliferation by LFA3TIP is due to its LFA-3 domain.

It will be recognized from the foregoing description that a wide variety of CD2-binding polypeptides in addition to those specifically mentioned, as well as fragments and analogues of such polypeptides, will be useful additional embodiments of the present invention. All such embodiments, and other embodiments that are obvious in view of the teachings herein, are specifically contemplated and are included within the scope of the invention as defined in the following claims.

Deposits

Host cells harboring plasmids bearing DNA sequences according to this invention were deposited under the Budapest Treaty with American Type Culture Collection (ATCC), Rockville, Maryland (USA) on March 5, 1991. The deposited cultures are identified as follows:

plasmid	host strain	Accession No.	Description: (plasmid contains DNA for:)
pPYM57	E.coli JA221	68545	M57 deletion mutant
pPMDRM54-6	E.coli JA221	68542	M54 deletion mutant
pPMDRM55-9	E.coli JA221	68546	M55 deletion mutant
pPMDRM56-C	E.coli JA221	68551	M56 deletion mutant
pPMDRM58-15	E.coli JA221	68547	M58 deletion mutant
pPYM63-4	E.coli JA221	68544	M63 deletion mutant
pPYM65-8	E.coli JA221	68552	M65 deletion mutant
pPMDRM100-4	E.coli JA221	68550	M100 deletion mutant
pPMDRM101-1	E.coli JA221	68543	M101 deletion mutant
pPMDRM102-8	E.coli JA221	68548	M102 deletion mutant
pPMDRM3-10	E.coli JA221	68549	PIM3 deletion mutant

A host cell harboring a plasmid according to this invention was deposited under the Budapest Treaty with the ATCC on October 1, 1991 is identified as follows:

plasmid	host strain	Accession No.	Description: (plasmid contains)
pSAB152	E.coli JA221	68720	Hybrid DNA sequence encoding LFA-3 signal sequence, N-terminal 92 amino acids of LFA-3, 10 amino acids of IgG1 hinge region, C_H2 and C_H3 IgG1 constant domains.

A bacteriophage and a bacterial strain carrying a vector referred to herein were deposited under the Budapest Treaty with In Vitro International, Inc., Linthicum, Maryland (USA) on May 28, 1987 and May 24, 1988, respectively, and assigned accession numbers IVI-10133 and IVI-10170, respectively. These deposits were transferred to the ATCC on June 20, 1991. The deposits are identified as:

Designation	Accession No.	Description
λHT16[λgt10/LFA-3]	75107	Contain DNA encoding full length transmembrane LFA-3
E.coli, BG8	68791	

The following hybridoma cell lines referred to herein were deposited under the Budapest Treaty with the ATCC on March 5, 1991:

Hybridoma	Accession No.	Antibody
7A6-2E5	HB 10695	7A6
1E6-2C12	HB 10693	1E6

While we have hereinbefore described a number of embodiments of this invention, it is apparent that our basic embodiments can be altered to provide other embodiments that utilize the compositions and processes of this invention. Therefore, it will be appreciated

that the scope of this invention includes all alternative embodiments and variations which are defined in the foregoing specification and by the claims appended hereto; and the invention is not to be limited by the specific embodiments that have been presented herein by way of example.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BIOGEN, INC.
WALLNER, Barbara P.
MILLER, Glenn T.
ROSA, Margaret D.

(ii) TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN 3

(iii) NUMBER OF SEQUENCES: 43

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(F) ZIP: 10022-6250

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(A) APPLICATION NUMBER: US 07/667,971
(B) FILING DATE: 12-MAR-1991

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/770,967
(B) FILING DATE: 07-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn Arg Val Tyr Leu Asp Thr Val Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His
1 5 10 15

Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys
20 25 30

Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser
35 40 45

Phe Lys
50

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Val Val Asp
1 5 10 15

Val Val Arg Asn
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val
1 5 10 15

Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln Ile
20 25 30

Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val
35 40 45

Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu
50 55 60

Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATAGGGTTT ATTTAGACAC TGTGTCAGGT 30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAATGGATTG CTAAGAAAGA ACTTCATGGT 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1040 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 10..759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CGACGAGCC ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC          48
          Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val
            1               5                  10

CTC AGC GTG GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT        96
Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
     15                  20                  25

TCC CAA CAA ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA       144
Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
 30                  35                  40                  45

CCA AGC AAT GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT       192
Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
                 50                  55                  60

AAA GTT GCA GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT       240
Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
               65                  70                  75

AAA AAT AGG GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC       288
Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
         80                  85                  90

AAC TTA ACA TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT       336
Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
     95                  100                 105

ATT ACT GAT ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA       384
Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
110                 115                 120                 125
```

```
TCT CCC ACA CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA        432
Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
                130                 135                 140

TGC ATG ATA CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC        480
Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr
            145                 150                 155

TCA TGG GAT TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA        528
Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile
        160                 165                 170

TAT TTT AAG ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT        576
Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu
    175                 180                 185

AGC AAT CCA TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT        624
Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys
190                 195                 200                 205

ATC CCA AGC AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA        672
Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile
                210                 215                 220

CCA TTA GCA GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT        720
Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile
            225                 230                 235

CTG AAA TGT GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGATTGGTAA        769
Leu Lys Cys Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
        240                 245                 250

CAGAAGATGA AGACAACAGC ATAACTAAAT TATTTTAAAA ACTAAAAAGC CATCTGATTT     829

CTCATTTGAG TATTACAATT TTTGAACAAC TGTTGGAAAT GTAACTTGAA GCAGCTGCTT     889

TAAGAAGAAA TACCCACTAA CAAAGAACAA GCATTAGTTT TGGCTGTCAT CAACTTATTA     949

TATGACTAGG TGCTTGCTTT TTTTGTCAGT AAATTGTTTT TACTGATGAT GTAGATACTT    1009

TTGTAAATAA ATGTAAATAT GTACACAAGT G                                   1040
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
1 5 10 15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
20 25 30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
165 170 175

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
180 185 190

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
195 200 205

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
210 215 220

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
225 230 235 240

Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
245 250

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 863 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 18..737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GCGGCCGCCG ACGAGCC ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG          50
                   Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu
                     1               5                  10

GGG GTC CTC AGC GTG GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC          98
Gly Val Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser
               15                  20                  25

TGT TTT TCC CAA CAA ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC         146
Cys Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe
          30                  35                  40

CAT GTA CCA AGC AAT GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA         194
His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln
     45                  50                  55

AAG GAT AAA GTT GCA GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA         242
Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser
 60                  65                  70                  75

TCT TTT AAA AAT AGG GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT         290
Ser Phe Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr
                 80                  85                  90

ATC TAC AAC TTA ACA TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG         338
Ile Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser
               95                  100                 105

CCA AAT ATT ACT GAT ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT         386
Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser
          110                 115                 120

CTT CCA TCT CCC ACA CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA         434
Leu Pro Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu
     125                 130                 135

GTC CAA TGC ATG ATA CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA         482
Val Gln Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile
140                 145                 150                 155

ATG TAC TCA TGG GAT TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC         530
Met Tyr Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr
                160                 165                 170
```

```
AGT ATA TAT TTT AAG ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT      578
Ser Ile Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys
            175                 180                 185

ACT CTT AGC AAT CCA TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA      626
Thr Leu Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr
        190                 195                 200

ACC TGT ATC CCA AGC AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA      674
Thr Cys Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile
    205                 210                 215

CCC ATA CCA TTA GCA GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT      722
Pro Ile Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn
220                 225                 230                 235

GGT ATG TAT GCT TTT TAAAACAAAA TAGTTTGAAA ACTTGCATTG TTTTCCAAAG      777
Gly Met Tyr Ala Phe
                240

GTCAGAAAAT AGTTTAAGGA TGAAAATAAA GTTTGAAATT TTAGACATTT GAAAAAAAAA    837

AAAAAAAAAA AAAAAAAAGC GGCCGC                                        863
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 1               5                  10                  15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
            20                  25                  30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
        35                  40                  45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
    50                  55                  60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65                  70                  75                  80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
                85                  90                  95
```

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
165 170 175

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
180 185 190

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
195 200 205

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
210 215 220

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTTTTAAA GGCACATACA CAACACCATA 30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACTTTATCC TTTTGATTGC TTGGTACATG 30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCTCTGAAT TCAGATTTTT TCCATAGGAC 30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAAATAAACC CTATTATTTT CCAGTTCTGC 30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGATAGTG AGGCTTTTAA AAGATGAGAA 30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACTCATCT TCATCACCTG ACACAGTGTC 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTATCAGTA ATATTTGATG ATGTTAAGTT 30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGACTCAAGC ACATATGGCG ATTCCATTTC 30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAATGCACAA GTTAGAAGAA AGAACTTCAT 30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATGCATTGG ACTTCTGTGG GAGATGGAAG 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCCTCGATGG CTGTTAATGC TTCCATTAGT 30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATAGGACAA TCCCAGTAAT GCTCTGGTAT 30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATACTGGTT GAGTTTGAGT ACATTATAAG 30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTGTGGAAGA TCATTACGTT TACATTGCTC 30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAATGGATTG CTAAGTTCCA TCTTAAAATA 30

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGTCAAAATG ATTGAAGTAC ACTGTATTTT 30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCTTGAATGA CCGCTTGATG TTGTATTAAA 30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATACTCATCT TCATCATACA CAACACCATA 30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATAGGACAA TCCCATGATG ATGTTAAGTT 30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCTTGAATGA CCGCTTGAGT ACATTATAAG 30

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu
1 5 10 15

Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 6..23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TCGTC GAC AAA ACT CAC ACA TGC C 24
Asp Lys Thr His Thr Cys
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp Lys Thr His Thr Cys
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTAAATGAGT GCGGCGGCCG CCAA 24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG ATCTGCAGCA 60

TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC 115

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 13..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAGGCGGCCG CC ATG GTT GCT GGG AGC GAC GCG 33
Met Val Ala Gly Ser Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Val Ala Gly Ser Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AAGTCGACAT AAAGAAAGAA CTTCAT 26

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCGACGCGGC CGCG

14

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG        48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 1               5                  10                  15

GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA        96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
            20                  25                  30

ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT       144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
        35                  40                  45

GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA       192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
    50                  55                  60

GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG       240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65                  70                  75                  80

GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA       288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
                85                  90                  95
```

```
TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT      336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
            100                 105                 110

ACC ATG AAG TTC TTT CTT TAT GTC GAC AAA ACT CAC ACA TGC CCA CCG      384
Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro
        115                 120                 125

TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC      432
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    130                 135                 140

CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA      480
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
145                 150                 155                 160

TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC      528
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                165                 170                 175

TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG      576
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
            180                 185                 190

GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC      624
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
        195                 200                 205

CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC      672
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    210                 215                 220

AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA      720
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
225                 230                 235                 240

GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT      768
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
                245                 250                 255

GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC      816
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            260                 265                 270

TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG      864
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        275                 280                 285

AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC      912
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    290                 295                 300

TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG      960
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
305                 310                 315                 320
```

```
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC      1008
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                325                 330                 335

ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGAGTGCGG               1050
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 1               5                  10                  15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
            20                  25                  30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
        35                  40                  45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
    50                  55                  60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65                  70                  75                  80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
                85                  90                  95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
            100                 105                 110

Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro
        115                 120                 125

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    130                 135                 140

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
145                 150                 155                 160

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                165                 170                 175

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
            180                 185                 190
```

```
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
        195                 200                 205

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    210                 215                 220

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
225                 230                 235                 240

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
                245                 250                 255

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            260                 265                 270

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        275                 280                 285

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    290                 295                 300

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
305                 310                 315                 320

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                325                 330                 335

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            340                 345
```

CLAIMS

We claim:

1. A polypeptide having the amino acid sequence: X_1-X_2-(SEQ ID NO:1) Asn Arg Val Tyr Leu Asp Thr Val Ser Gly-Y, wherein:

X_1 is hydrogen or methionyl;

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy-terminal 1 to 77 amino acids of the sequence (SEQ ID NO:5): Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino terminal 1 to 32 amino acids of the sequence (SEQ ID NO:33): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val;

and analogs and derivatives thereof,

said polypeptide being capable of binding to CD2.

2. The polypeptide according to claim 1 wherein,

X_2, if present, is a polypeptide having the following amino acid sequence or a portion thereof consisting of the carboxy terminal 1 to 50 amino acids of the sequence (SEQ ID NO:2): Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys

Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys;

Y is hydroxyl or a polypeptide of the following amino acid sequence or a portion thereof consisting of the amino-terminal 1 to 10 amino acids of the sequence (SEQ ID NO:3): Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser;

and analogs and derivatives thereof,

said polypeptide being capable of binding to CD2.

3. The polypeptide according to claim 1, selected from the group consisting of polypeptides having the amino acid sequences: amino acids 29-120 of SEQ ID NO:10, amino acids 29-108 of SEQ ID NO:10, amino acids 48-108 of SEQ ID NO:10, and SEQ ID NO:7.

4. The polypeptide according to claim 2 having the amino acid sequence (SEQ ID NO:7): Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr.

5. An isolated DNA sequence encoding a polypeptide of any of claims 1, 2, 3 or 4.

6. An isolated DNA sequence encoding the CD2-binding domain of LFA-3 comprising:

(5') (SEQ ID NO:6) AATAGGGTTT ATTTAGACAC TGTGTCAGGT (3').

7. An isolated DNA sequence comprising a DNA sequence encoding the CD2-binding domain of LFA-3 selected from the group consisting of the DNA inserts of pPYM57, pPMDRM54-6, pPMDRM55-9, pPMDRM56-C, pPMDRM58-15, pPYM63-4, pPYM65-8, pPMDRM100-4, pPMDRM101-1, pPMDRM102-8, and pPMDRM3-10.

8. A recombinant DNA molecule comprising a DNA sequence according to claim 5, 6 or 7 and an expression control sequence, wherein the expression control sequence is operatively linked to the DNA sequence.

9. A fusion protein, having an amino terminal region characterized by the amino acid sequence of the polypeptides of any one of claims 1-4 and having a carboxy terminal region comprising a domain of a protein or polypeptide other than LFA-3.

10. The fusion protein according to claim 9 wherein the carboxy terminal region comprises at least a portion of the Fc region of an immunoglobulin.

11. The fusion protein according to claim 10 wherein the portion of the Fc region of an immunoglobulin comprises a hinge region and C_H2 and C_H3 constant domains.

12. The fusion protein according to claim 10 wherein the portion of the Fc region comprises a portion of a hinge region that is capable of forming intermolecular disulfide bonds and C_H2 and C_H3 constant domains.

13. The fusion protein according to claim 12 which is amino acids 29-347 of SEQ ID NO:43.

14. An isolated DNA sequence coding for a fusion protein according to any one of claims 9-13.

15. A recombinant DNA molecule comprising the DNA sequence according to claim 14 and an expression control sequence, wherein the expression control sequence is operatively linked to the DNA sequence.

16. The recombinant DNA molecule, according to claim 15, selected from the group consisting of plasmid pSAB152 and plasmid pMDR(92)Ig-3.

17. A multimeric protein capable of binding to CD2 comprising (a) two or more polypeptides according to any one of claims 1-4, (b) two or more fusion proteins according to any one of claims 9-13, or (c) one or more polypeptides according to any one of claims 1-4 and one or more fusion proteins according to any one of claims 9-13.

18. A method for producing a protein comprising the step of culturing a host cell transformed with the recombinant DNA molecule of claim 8, 15 or 16.

19. A host cell transformed with the recombinant DNA molecule according to claim 8, 15 or 16.

20. A method for labeling $CD2^+$ cells or proteins containing the LFA-3 binding domain of CD2, said method comprising the step of incubating the $CD2^+$ cells or proteins containing the LFA-3 binding domain of CD2 with a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13.

21. A method for clearing solutions, including sera, of anti-LFA-3 antibodies recognizing LFA-3 epitopes other than the CD2-binding domain of LFA-3 comprising the steps of contacting the solution of anti-LFA-3 antibodies with an LFA-3 deletion mutant protein selected from M57, M55, M56, PIM3, M100, or combinations thereof, under conditions suitable for forming antibody-protein complexes, then removing any antibody-protein complexes formed from said solution.

22. A method for isolating $CD2^+$ cells or proteins having the LFA-3-binding domain of CD2 comprising the steps of coupling a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13 to a chromatographic substrate and contacting a cell suspension containing $CD2^+$ cells or a solution containing proteins having the LFA-3-binding domain of CD2 with said substrate under conditions suitable for the formation of a LFA-3/CD2 complex.

23. A pharmaceutical composition comprising a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13, and a pharmaceutically acceptable carrier.

24. A diagnostic kit for detecting the presence of $CD2^+$ cells or LFA-3-binding proteins comprising a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13, as a reagent.

25. The use of a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13 to inhibit T-cell activation.

26. The use of a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 16-19 to inhibit proliferation of peripheral blood lymphocytes.

27. A method for initiating T-lymphocyte responses in vivo comprising administering to a mammal a polypeptide according to any one of claims 1-4 or a fusion protein according to any one of claims 9-13.

FIG. 1A-1

```
1    CGACGAGCCATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCT   50
          MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLe
          -28

51   CAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTCATCAGCTGTTTTTCCC  100
     uSerValValCysLeuLeuHisCysPheGlyPheIleSerCysPheSerG    3
                                                    +1

101  AACAAATATATGGTGTTGTGTATGGGAATGTAACTTTCCATGTACCAAGC  150
     lnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSer   19
                                  M53

151  AATGTGCCTTTAAAAGAGGTCCTATGGAAAAAACAAAAGGATAAAGTTGC  200
     AsnValProLeuLysGluValLeuTrpLysLysGlnLysAspLysValAl   36
                        M54                       M55

201  AGAACTGGAAAATTCTGAATTCAGAGCTTTCTCATCTTTTAAAAATAGGG  250
     aGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgV   53
                        M56

251  TTTATTTAGACACTGTGTCAGGTAGCCTCACTATCTACAACTTAACATCA  300
     alTyrLeuAspThrValSerGlySerLeuThrIleTyrAsnLeuThrSer   69
               M57                       M58
```

```
301  TCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACTGATACCAT   350
     SerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMe    86
                  M59                          M60

351  GAAGTTCTTTCTTTATGTGCTTGAGTCTCTTCCATCTCCCACACTAACTT   400
     tLysPhePheLeuTyrValLeuGluSerLeuProSerProThrLeuThrC   103
                        M61

401  GTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAGCAT   450
     ysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGluHis   119
            M62                          M63

451  TACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGTCCTATGGA   500
     TyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGl   136
                  M64                          M65

501  GCAATGTAAACGTAACTCAACCAGTATATATTTTAAGATGGAAAATGATC   550
     uGlnCysLysArgAsnSerThrSerIleTyrPheLysMetGluAsnAspL   153
                        M66
```

FIG. 1A-2

FIG. 1B

```
551   TTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTTAATACAACA   600
      euProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThr   169
            M90                                  M91

601   TCATCAATCATTTTGACAACCTGTATCCCAAGCAGCGGTCATTCAAGACA   650
      SerSerIleIleLeuThrThrCysIleProSerSerGlyHisSerArgHi   186
                  M92

651   CAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTATTG   700
      sArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleV   203
                        Transmembrane

701   TGCTGTATATGAATGGTATTCTGAAATGTGACAGAAAACCAGACAGAACC   750
      alLeuTyrMetAsnGlyIleLeuLysCysAspArgLysProAspArgThr   219

751   AACTCCAATTGATTGGTAACAGAAGATGAAGACAACAGCATAACTAAATT   800
      AsnSerAsn                                            222

801   ATTTTAAAAACTAAAAAGCCATCTGATTTCTCATTTGAGTATTACAATTT   850

851   TTGAACAACTGTTGGAAATGTAACTTGAAGCAGCTGCTTTAAGAAGAAAT   900

901   ACCCACTAACAAAGAACAAGCATTAGTTTTGGCTGTCATCAACTTATTAT   950

951   ATGACTAGGTGCTTGCTTTTTTTGTCAGTAAATTGTTTTTACTGATGATG   1000

1001  TAGATACTTTTGTAAATAAATGTAAATATGTACACAAGTG   1040
```

FIG. 2A

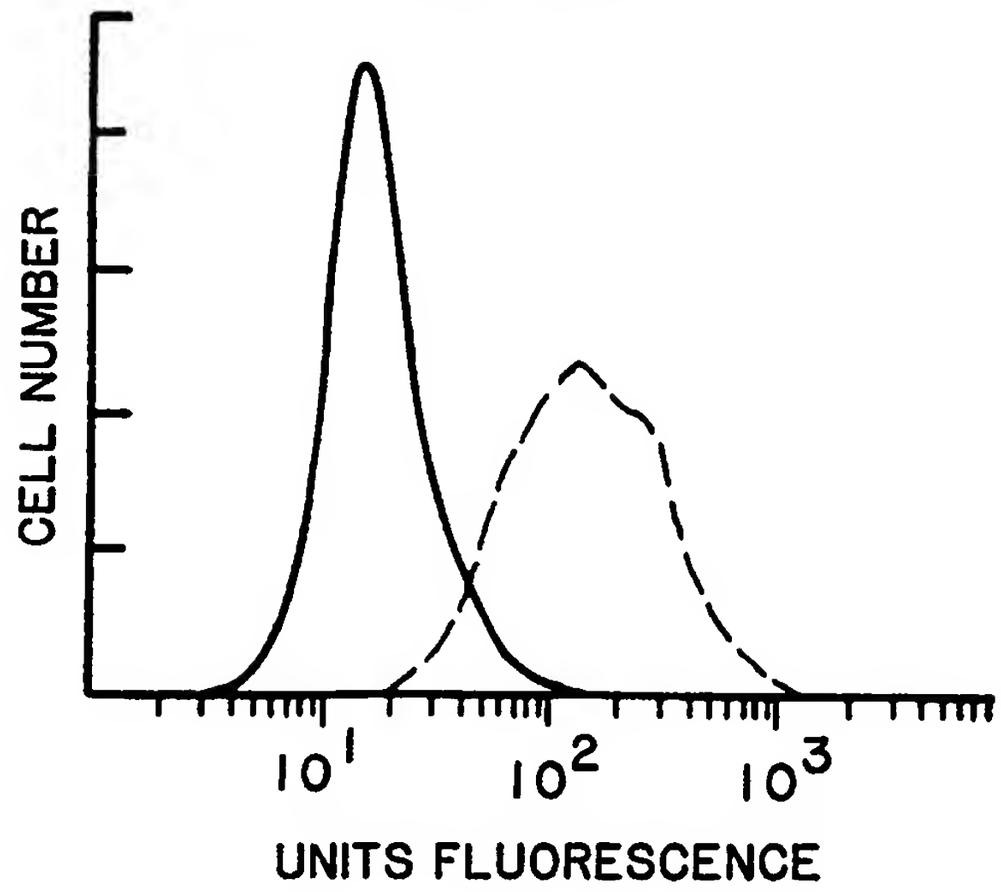
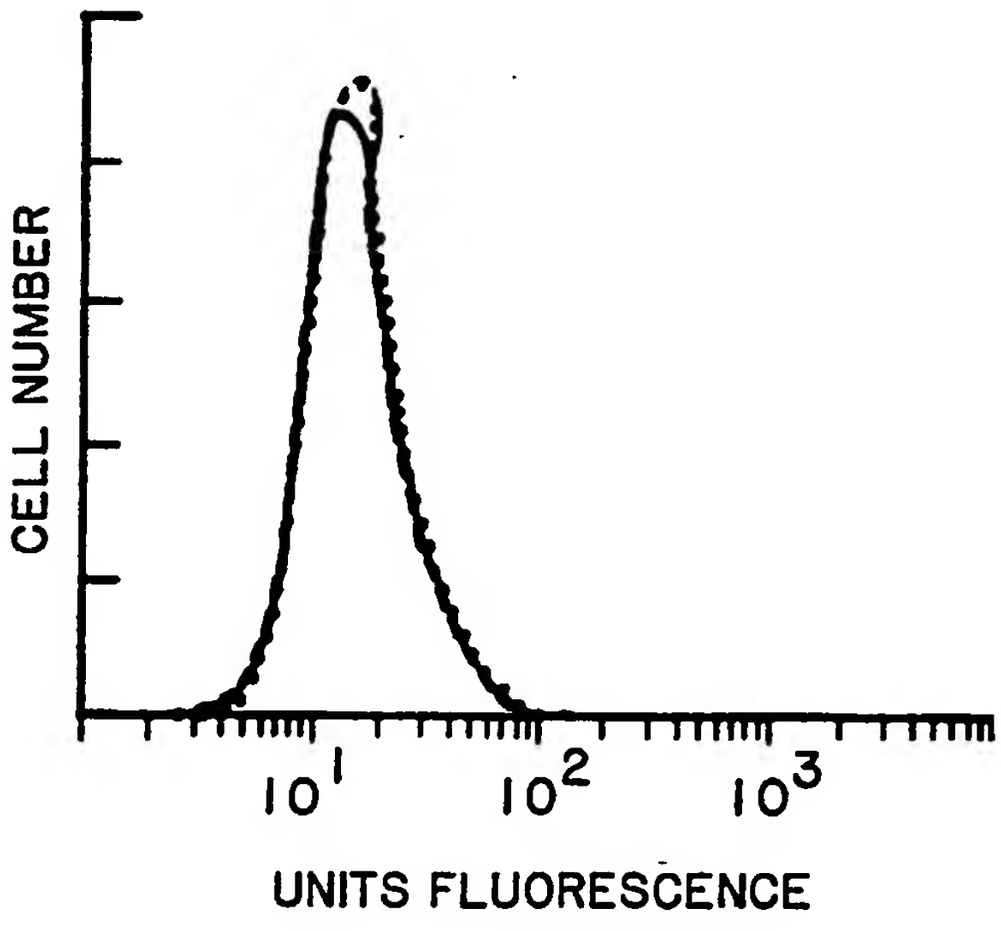

CELL NUMBER
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2B


CELL NUMBER
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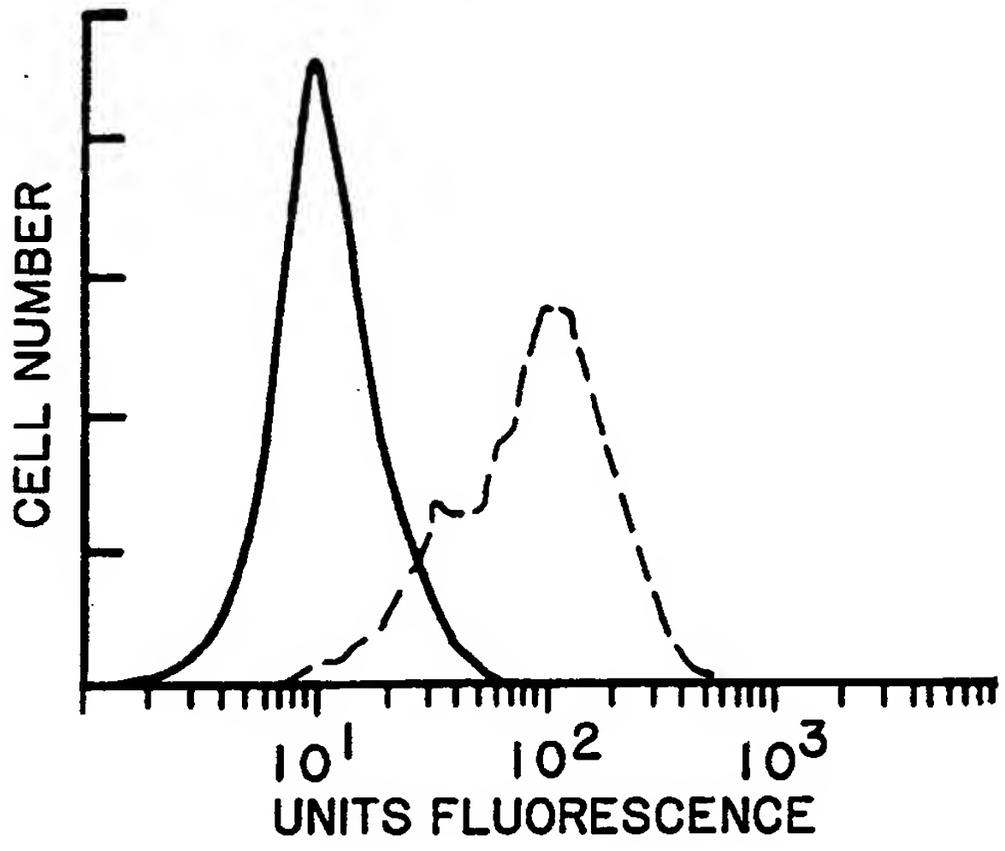
10^2
10^3
UNITS FLUORESCENCE

FIG. 2C


CELL NUMBER
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10^2
10^3
UNITS FLUORESCENCE

FIG. 2D

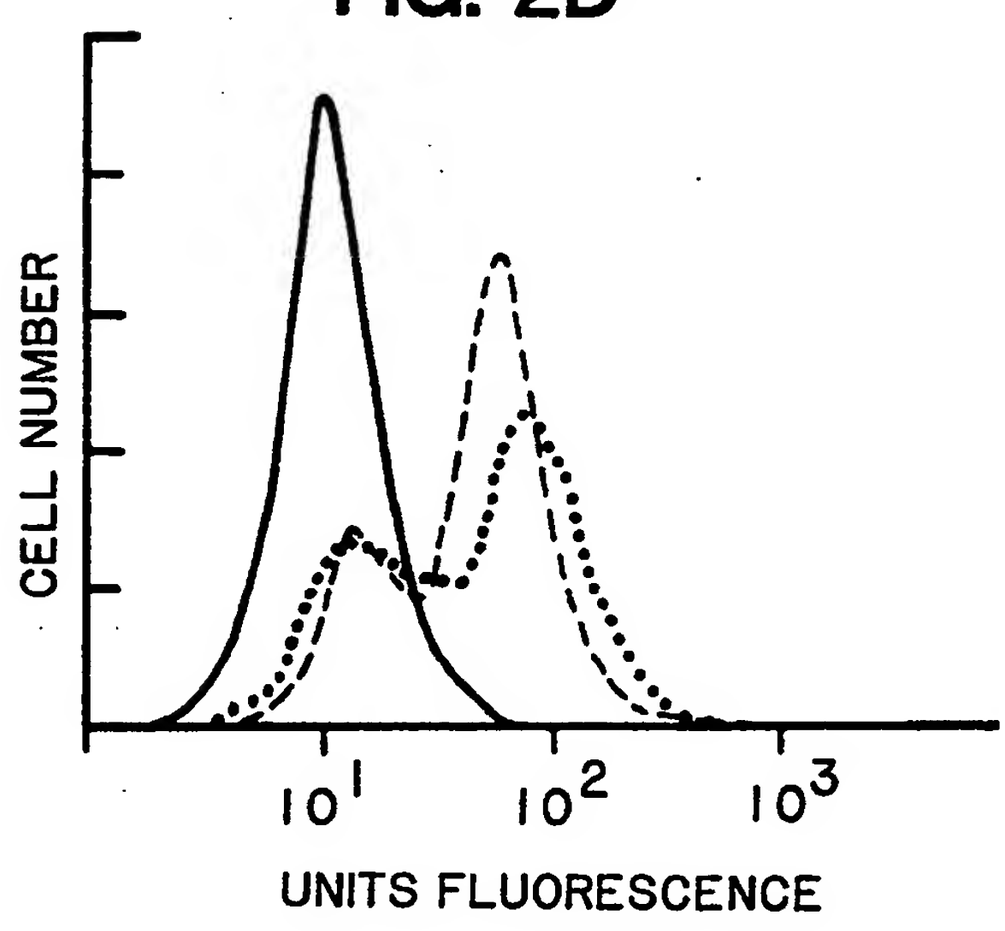
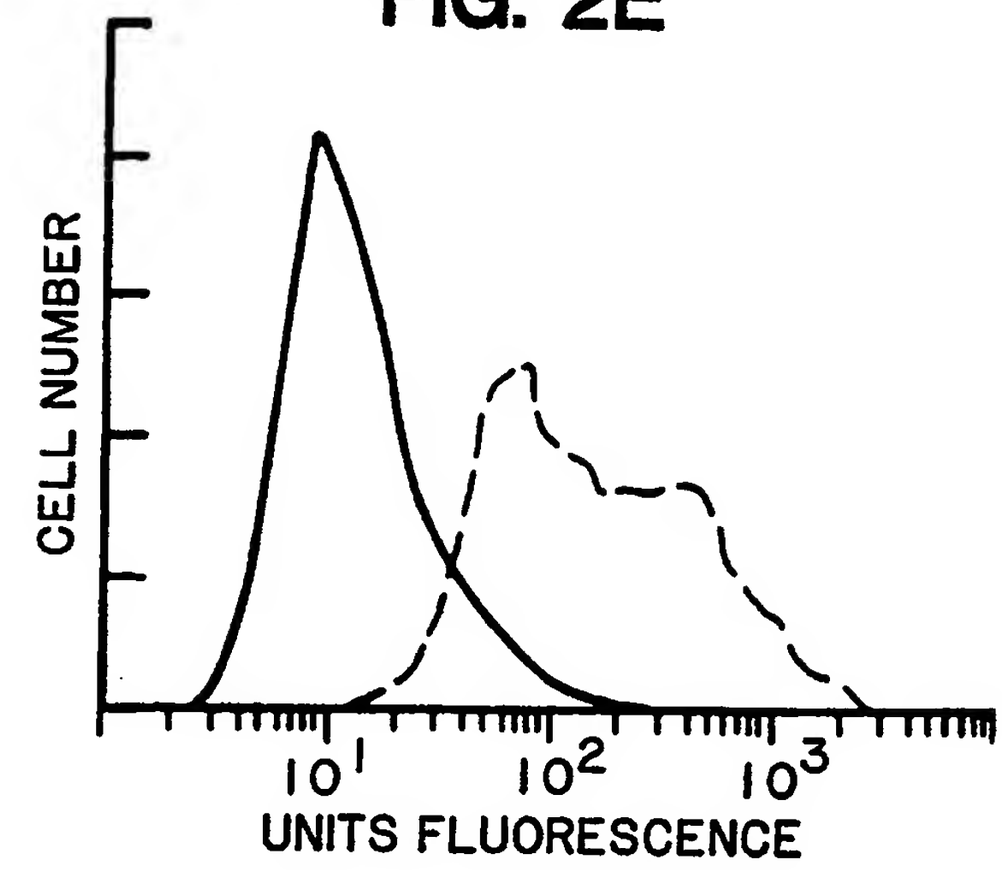

CELL NUMBER
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2E


CELL NUMBER
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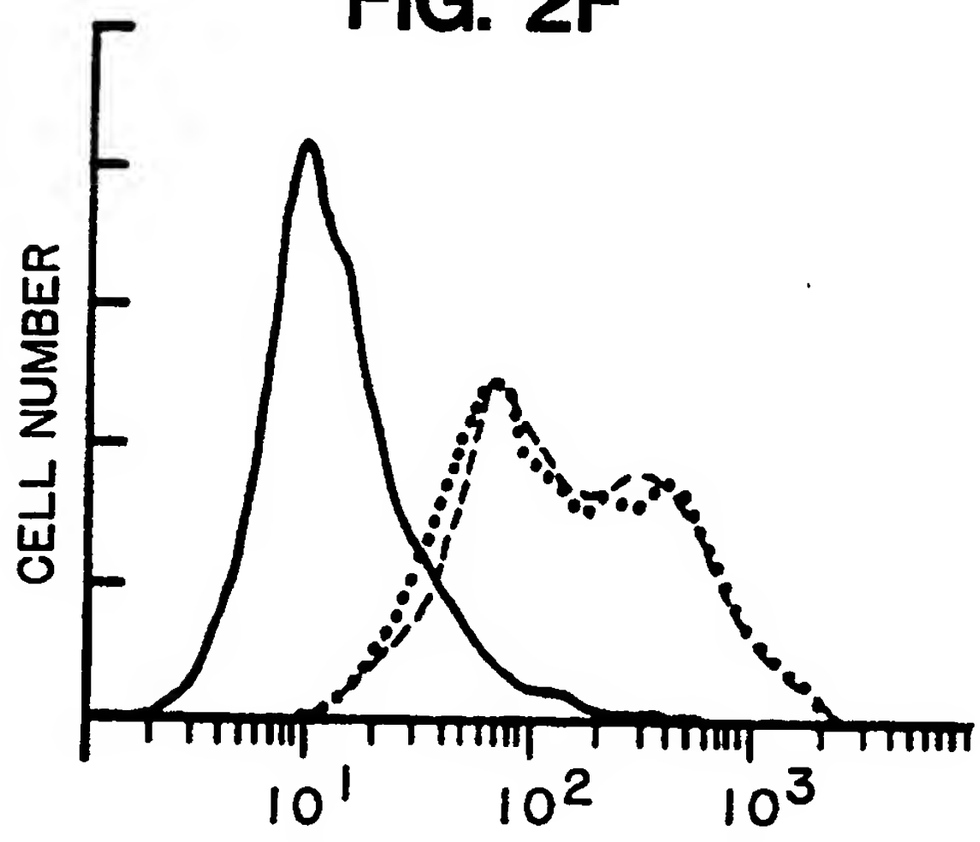
10^2
10^3
UNITS FLUORESCENCE

FIG. 2F


CELL NUMBER
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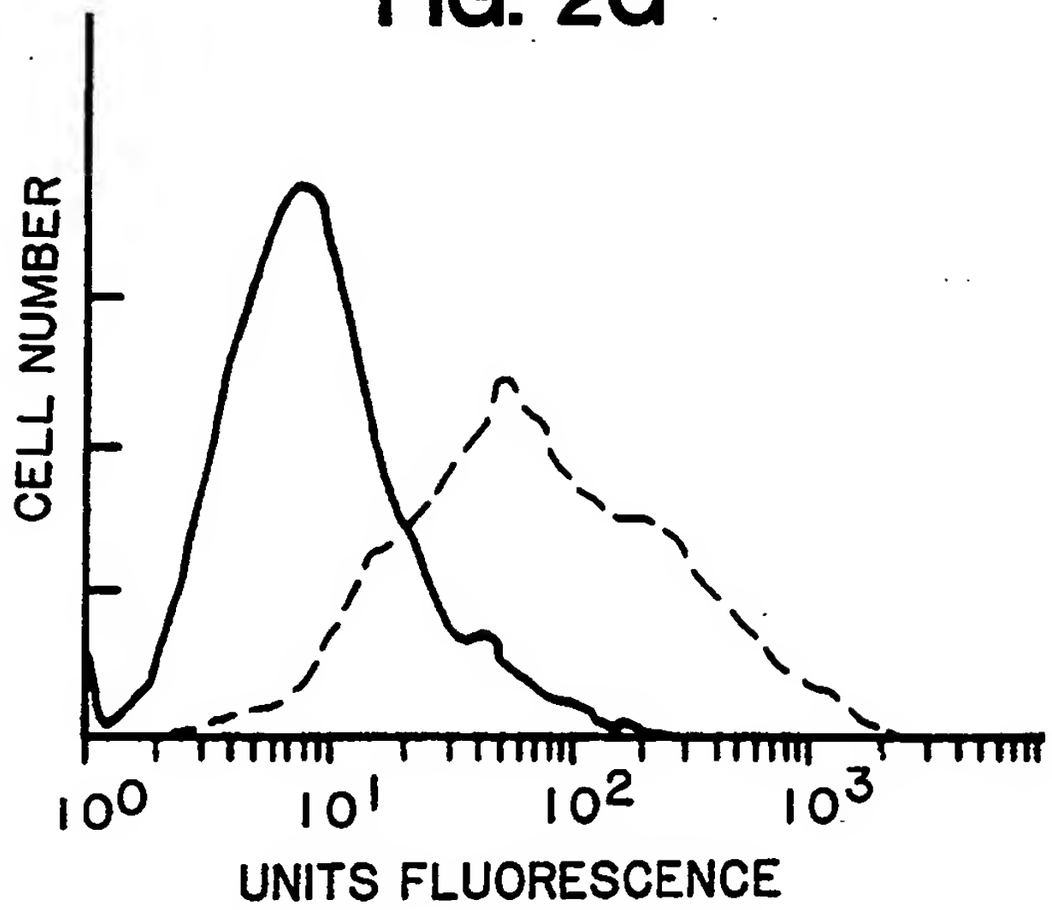
10^2
10^3
UNITS FLUORESCENCE

FIG. 2G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UNITS FLUORESCENCE

FIG. 2H

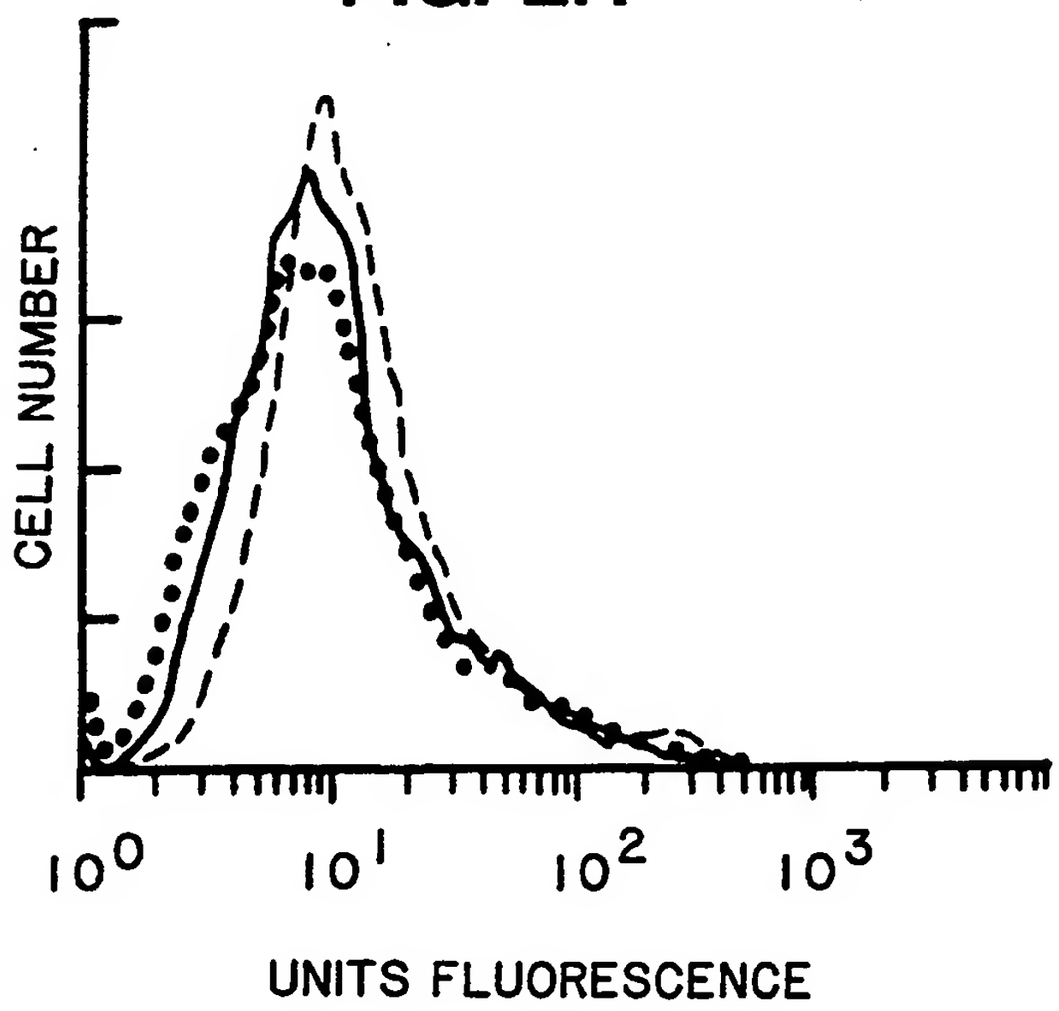

CELL NUMBER
10^0
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2I

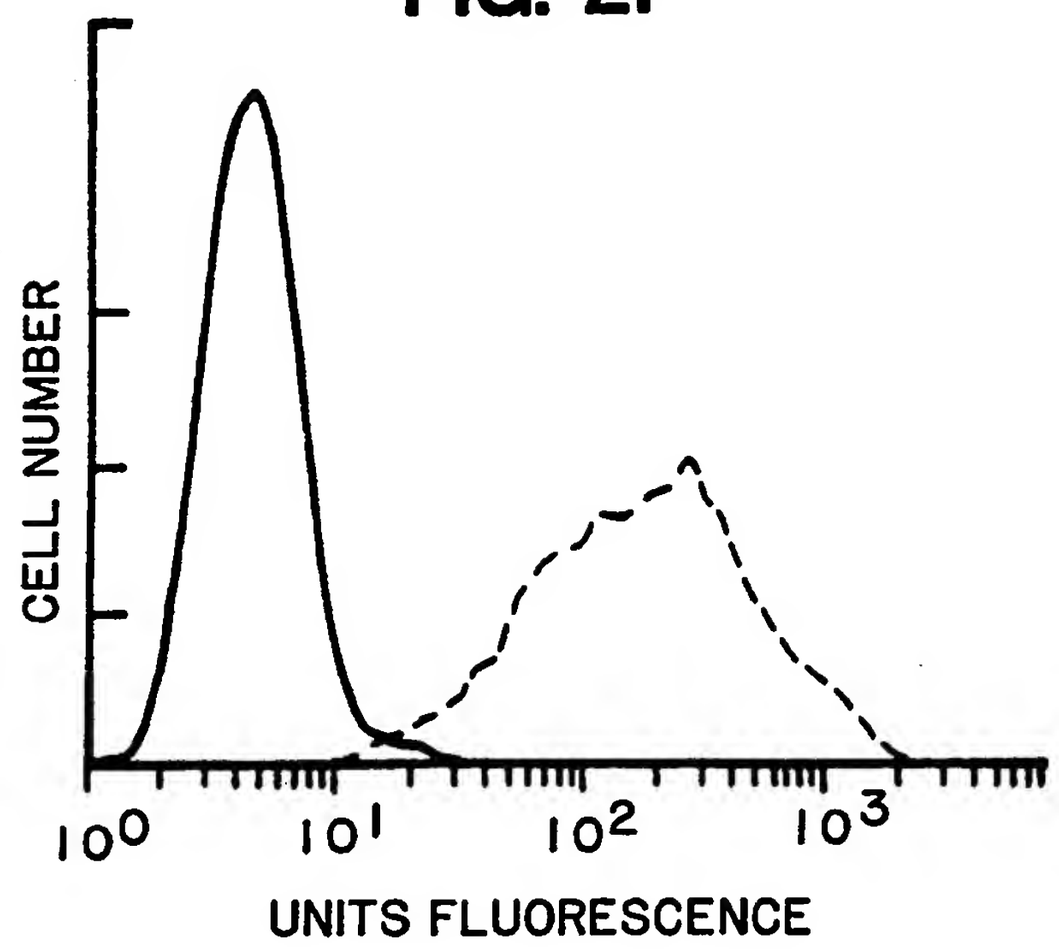
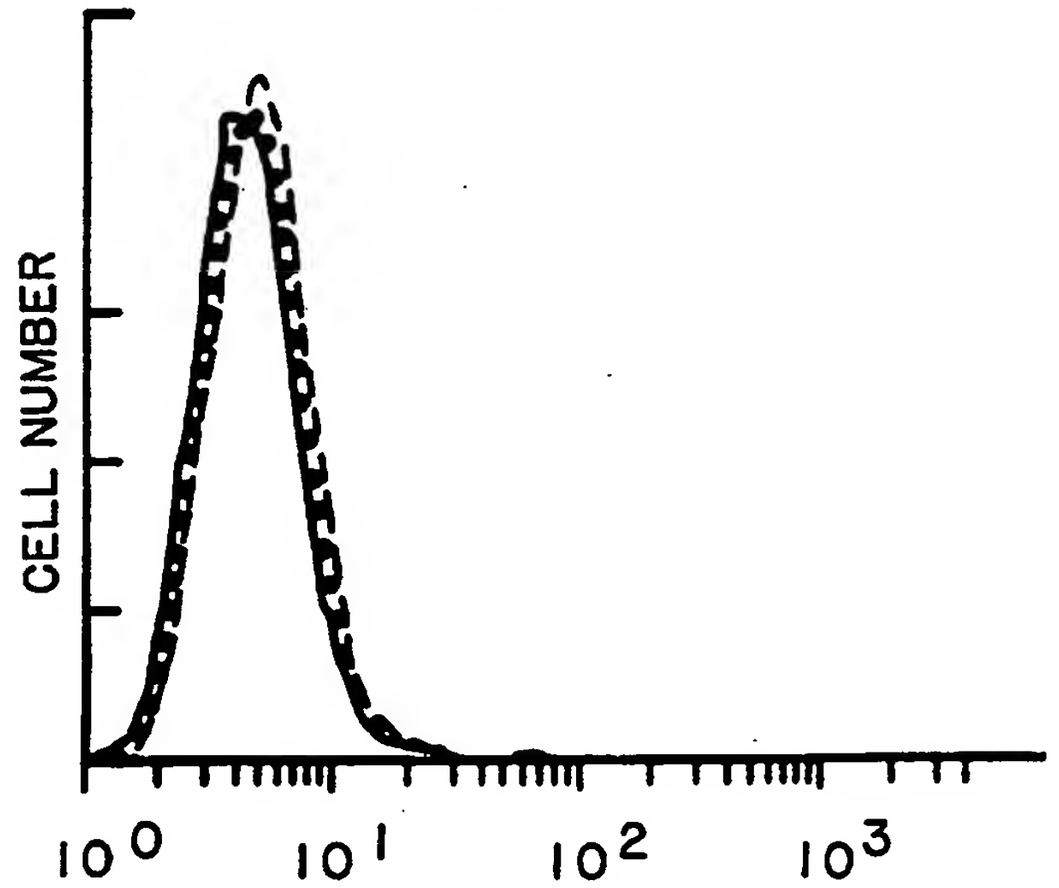

CELL NUMBER
10^0
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2J


CELL NUMBER
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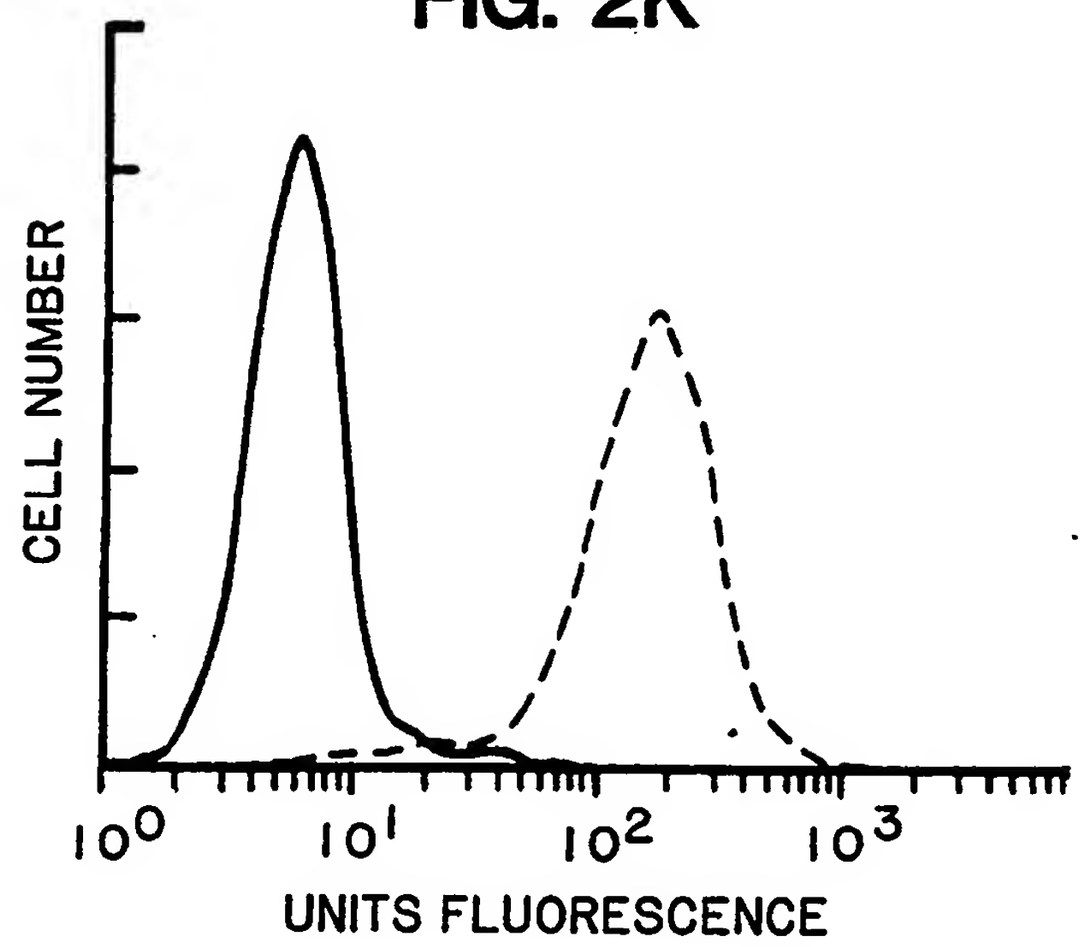
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2K


CELL NUMBER
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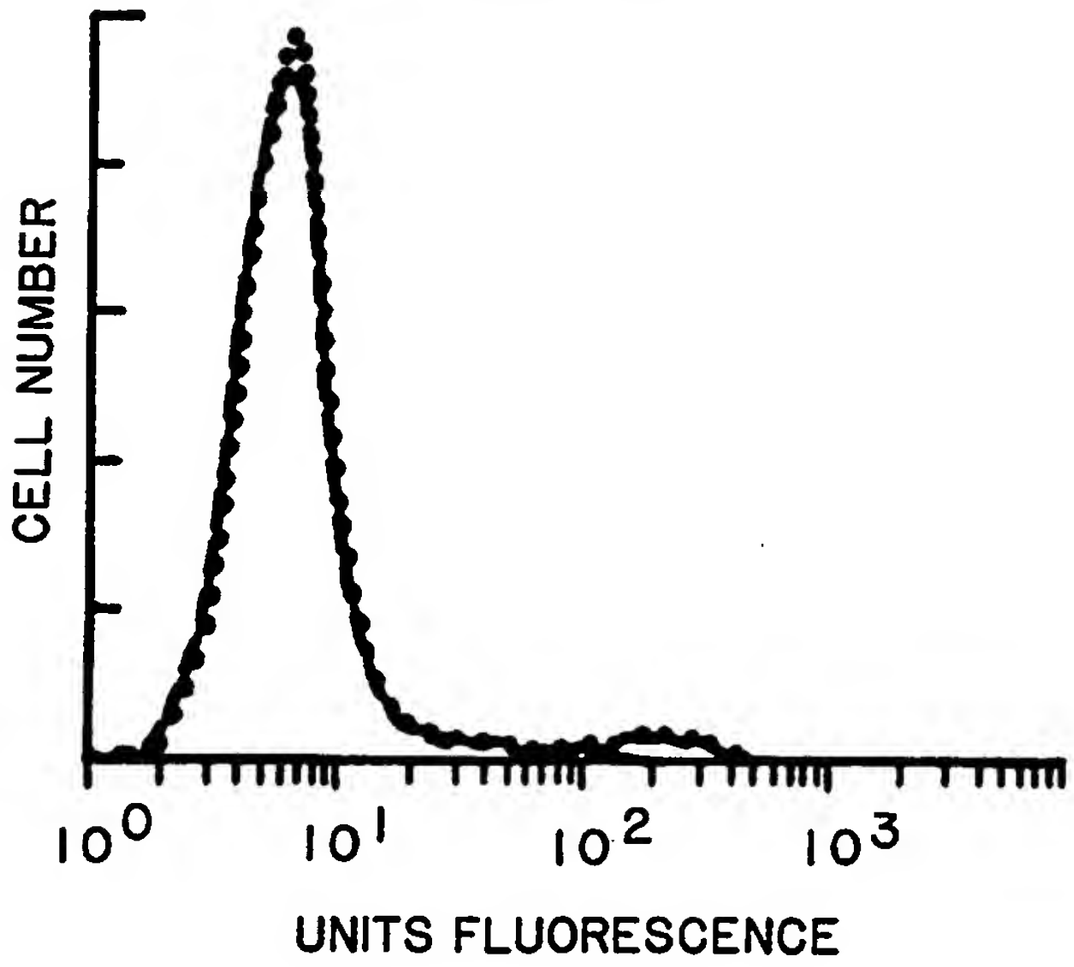
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2L


CELL NUMBER
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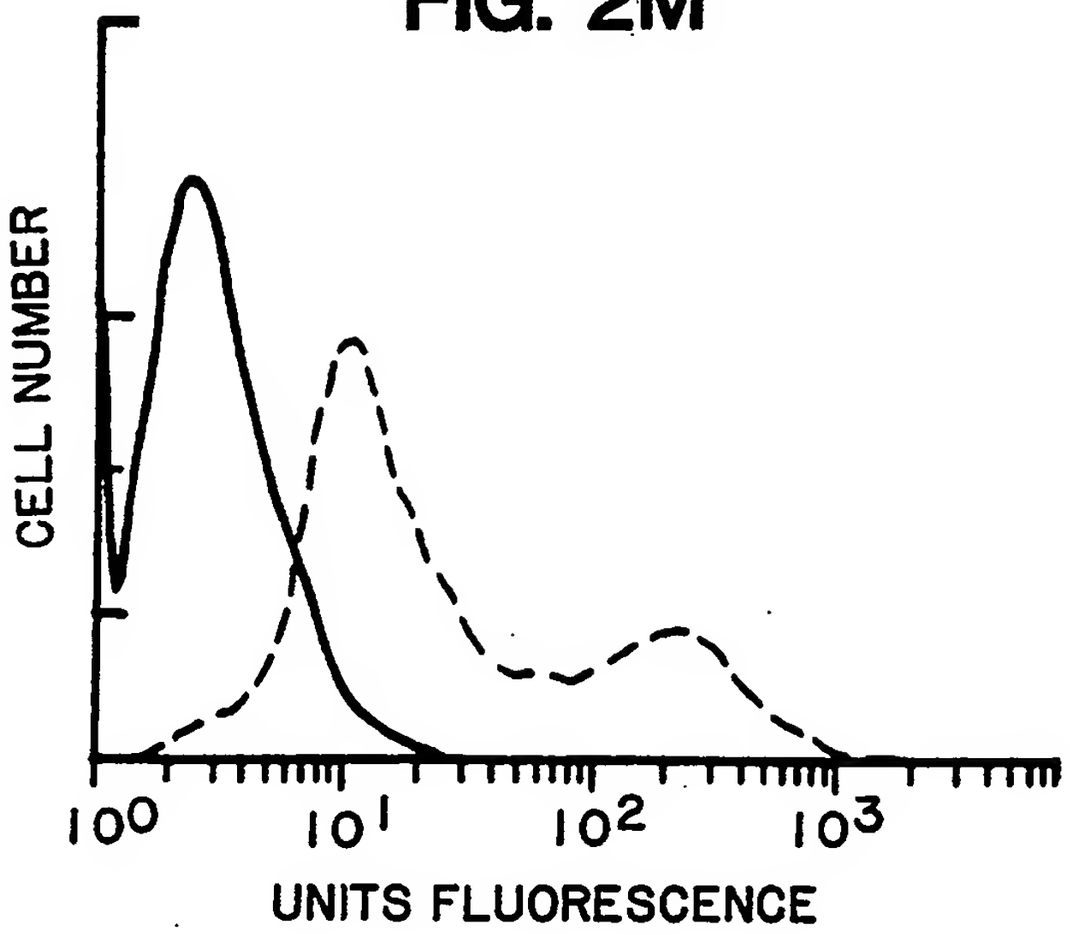
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2M


CELL NUMBER
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10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 2N

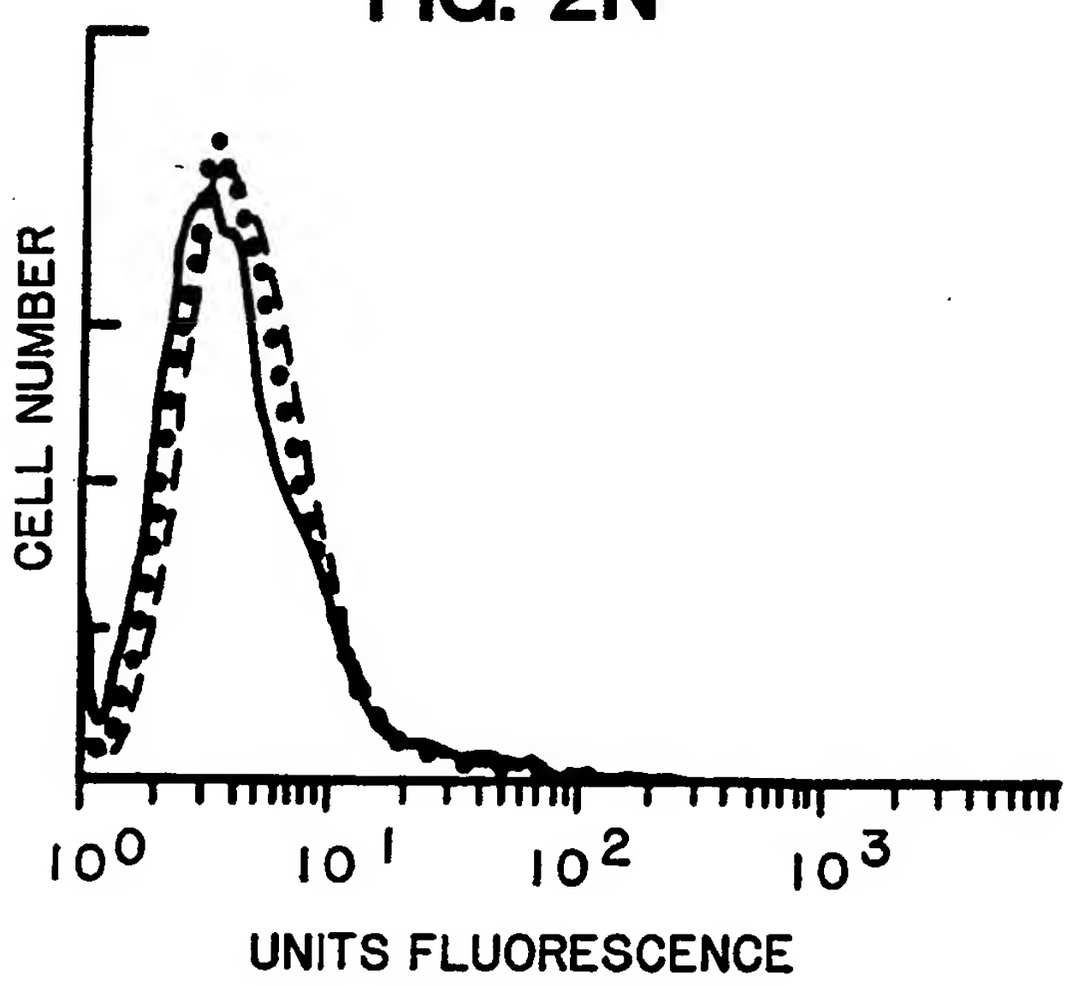

CELL NUMBER
10^0
10^1
10^2
10^3
UNITS FLUORESCENCE

FIG. 3A

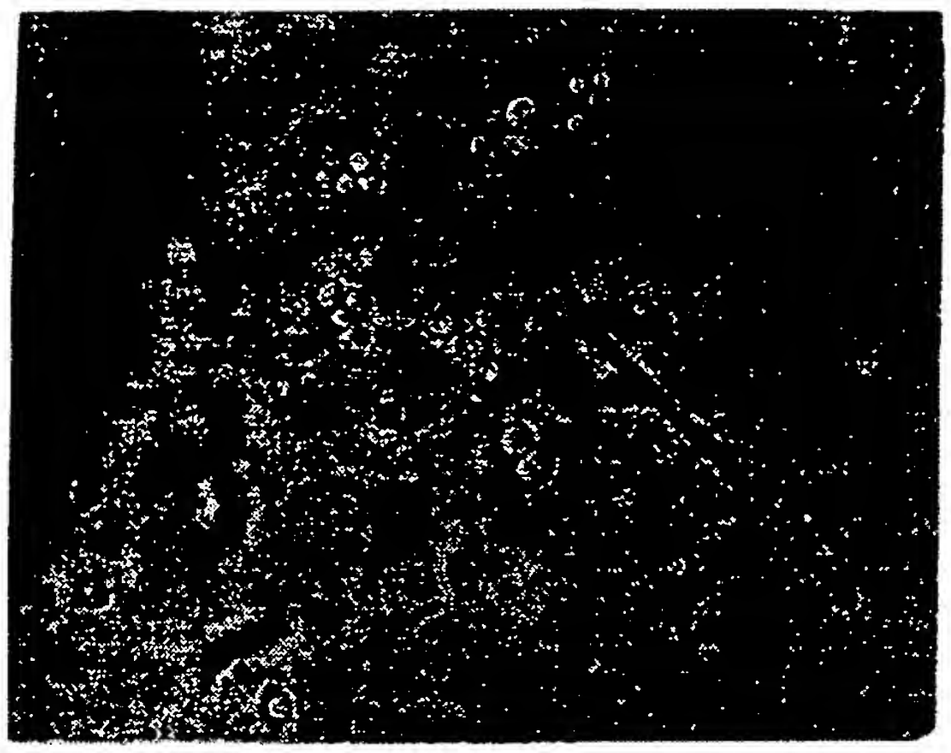


FIG. 3B

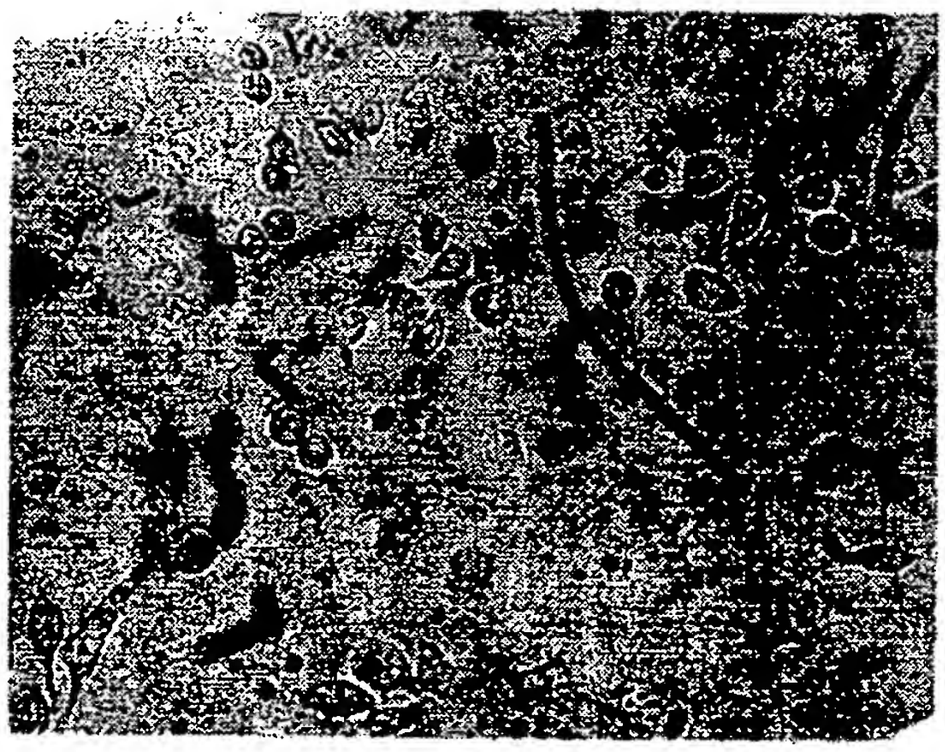


FIG. 3C

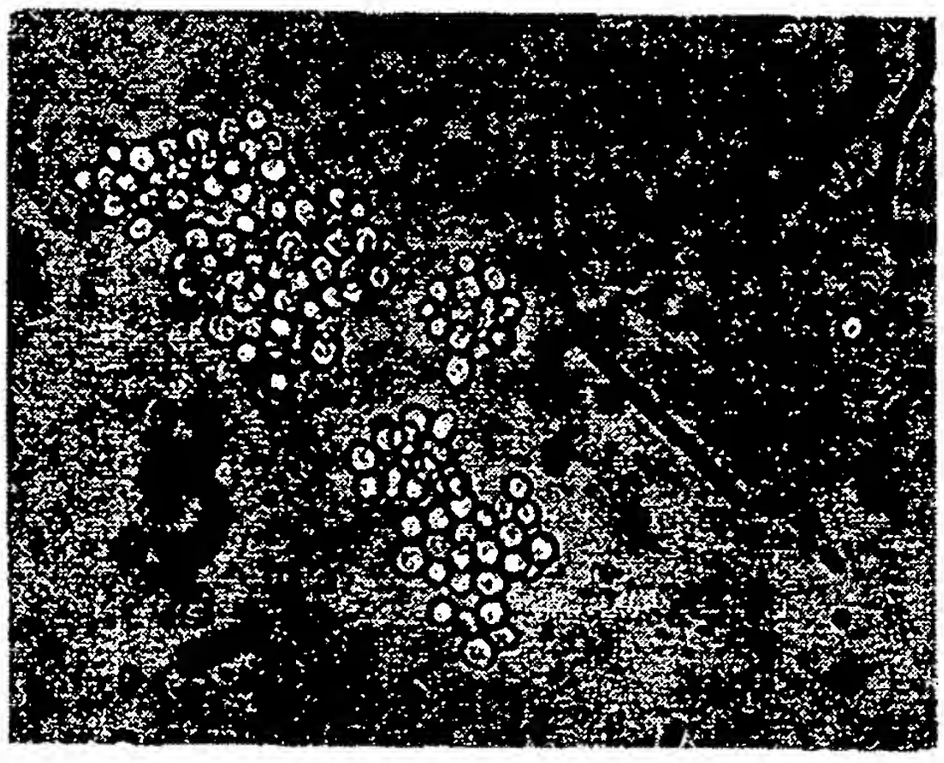


FIG. 4

CHO M57 M16,3

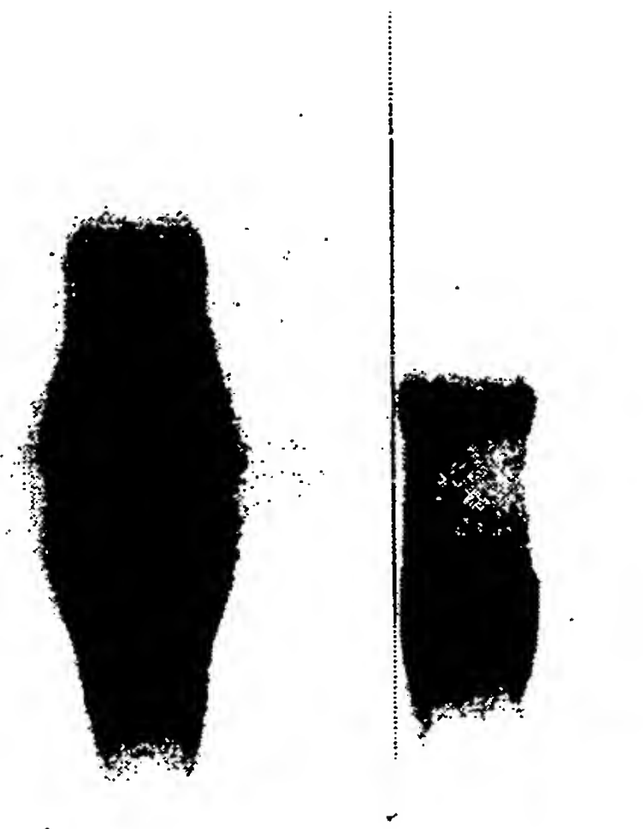


FIG. 5

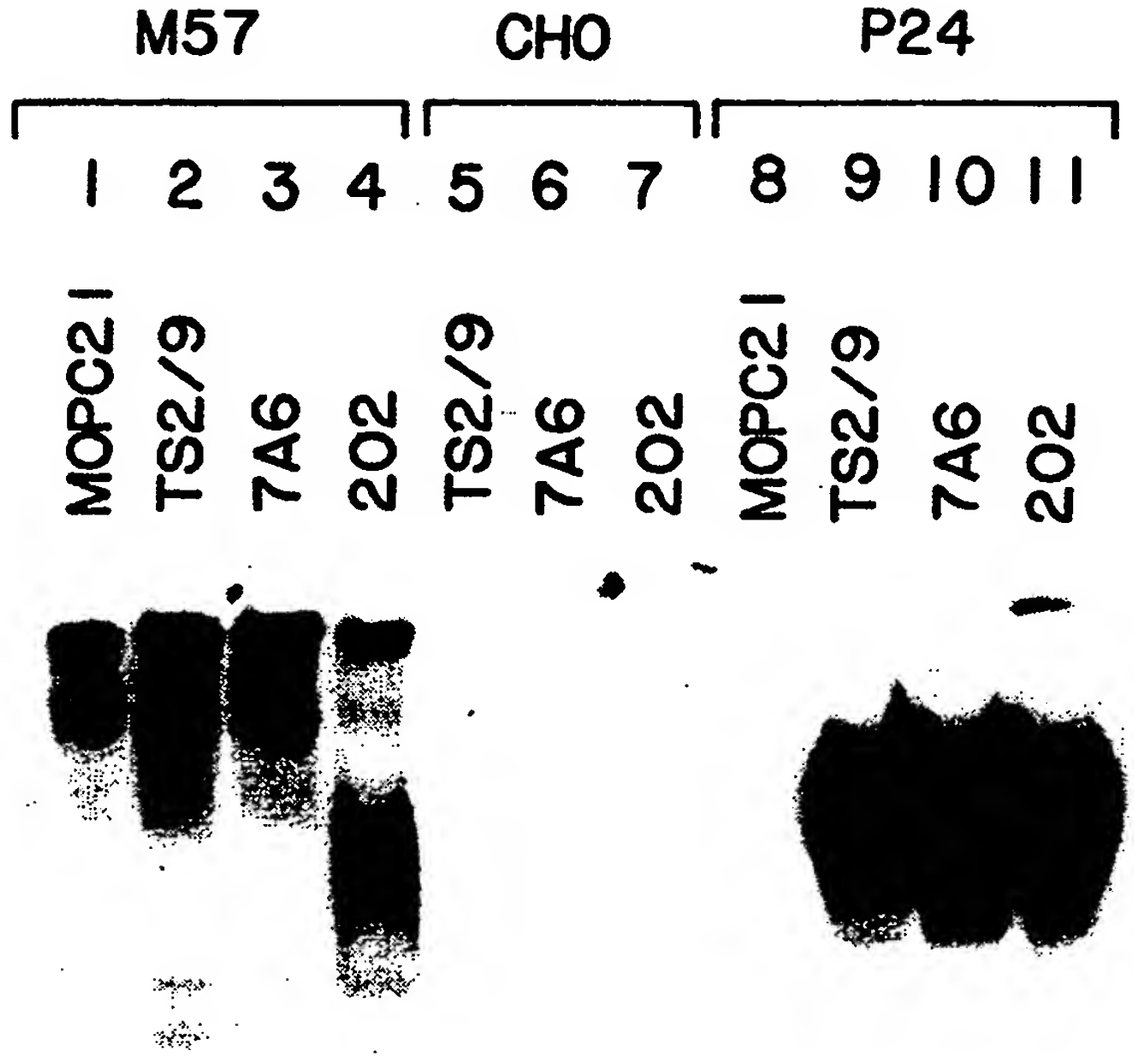

M57
CHO
P24
1 2 3 4 5 6 7 8 9 10 11
MOPC21
TS2/9
7A6
202
TS2/9
7A6
202
MOPC21
TS2/9
7A6
202

FIG. 6A-1

```
1    CGACGAGCCATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCT    50
              MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLe
              -28

51   CAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTCATCAGCTGTTTTTCCC   100
     uSerValValCysLeuLeuHisCysPheGlyPheIleSerCysPheSerG     3
                                                    +1

101  AACAAATATATGGTGTTGTGTATGGGAATGTAACTTTCCATGTACCAAGC   150
     lnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSer
                                                          19

151  AATGTGCCTTTAAAAGAGGTCCTATGGAAAAAACAAAAGGATAAAGTTGC   200
     AsnValProLeuLysGluValLeuTrpLysLysGlnLysAspLysValAl
                                                          36

201  AGAACTGGAAAATTCTGAATTCAGAGCTTTCTCATCTTTTAAAAATAGGG   250
     aGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgV    53
                    M 100

251  TTTATTTAGACACTGTGTCAGGTAGCCTCACTATCTACAACTTAACATCA   300
     alTyrLeuAspThrValSerGlySerLeuThrIleTyrAsnLeuThrSer    69
```

```
301  TCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACTGATACCAT   350
     SerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMe    86

351  GAAGTTCTTTCTTTATGTGCTTGAGTCTCTTCCATCTCCCACACTAACTT   400
     tLysPhePheLeuTyrValLeuGluSerLeuProSerProThrLeuThrC   103
                          M 101

401  GTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAGCAT   450
     ysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGluHis   119

451  TACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGTCCTATGGA   500
     TyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGl   136

501  GCAATGTAAACGTAACTCAACCAGTATATATTTTAAGATGGAAAATGATC   550
     uGlnCysLysArgAsnSerThrSerIleTyrPheLysMetGluAsnAspL   153
                          M 102
```

FIG. 6A-2

FIG. 6B

```
551   TTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTTAATACAACA   600
      euProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThr   169

601   TCATCAATCATTTTGACAACCTGTATCCCAAGCAGCGGTCATTCAAGACA   650
      SerSerIleIleLeuThrThrCysIleProSerSerGlyHisSerArgHi   186

651   CAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTATTG   700
      sArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleV   203

701   TGCTGTATATGAATGGTATTCTGAAATGTGACAGAAAACCAGACAGAACC   750
      alLeuTyrMetAsnGlyIleLeuLysCysAspArgLysProAspArgThr   219

751   AACTCCAATTGATTGGTAACAGAAGATGAAGACAACAGCATAACTAAATT   800
      AsnSerAsn                                           222

801   ATTTTAAAAACTAAAAAGCCATCTGATTTCTCATTTGAGTATTACAATTT   850

851   TTGAACAACTGTTGGAAATGTAACTTGAAGCAGCTGCTTTAAGAAGAAAT   900

901   ACCCACTAACAAAGAACAAGCATTAGTTTTGGCTGTCATCAACTTATTAT   950

951   ATGACTAGGTGCTTGCTTTTTTTGTCAGTAAATTGTTTTTACTGATGATG   1000

1001  TAGATACTTTTGTAAATAAATGTAAATATGTACACAAGTG             1040
```

FIG. 7A

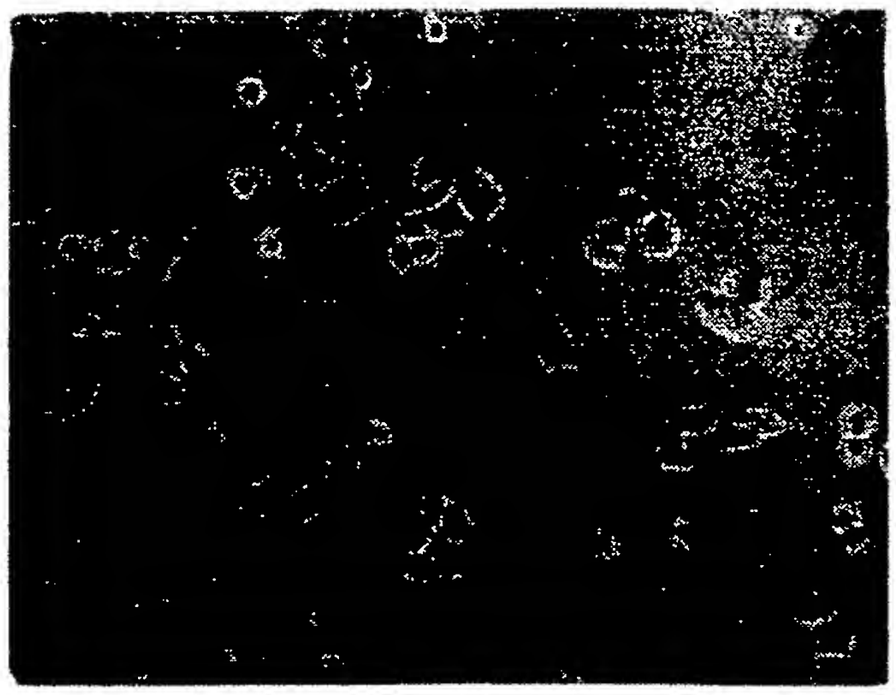


FIG. 7B

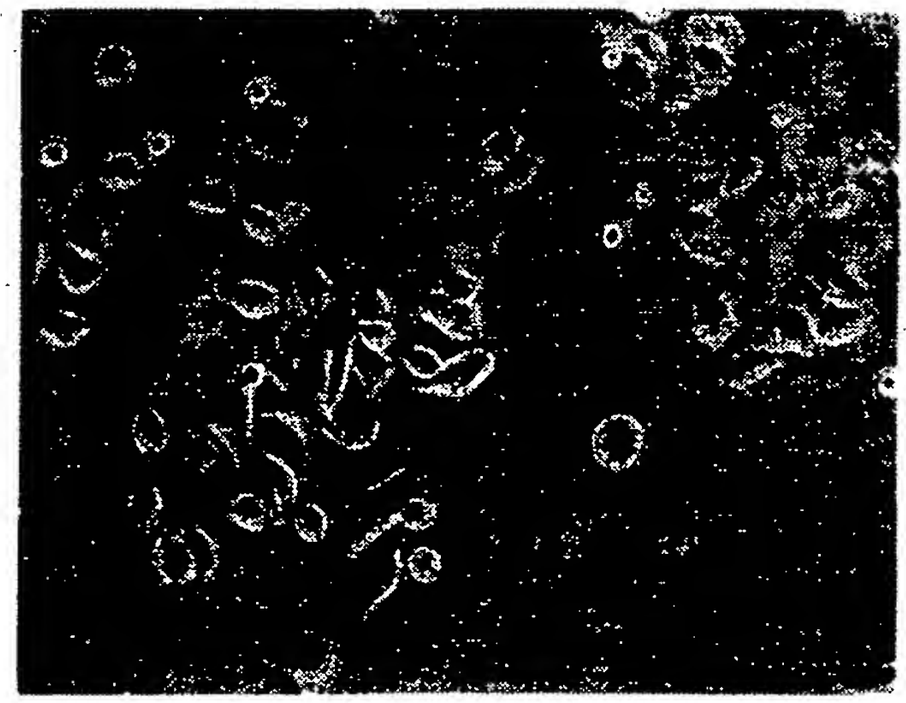


FIG. 7C

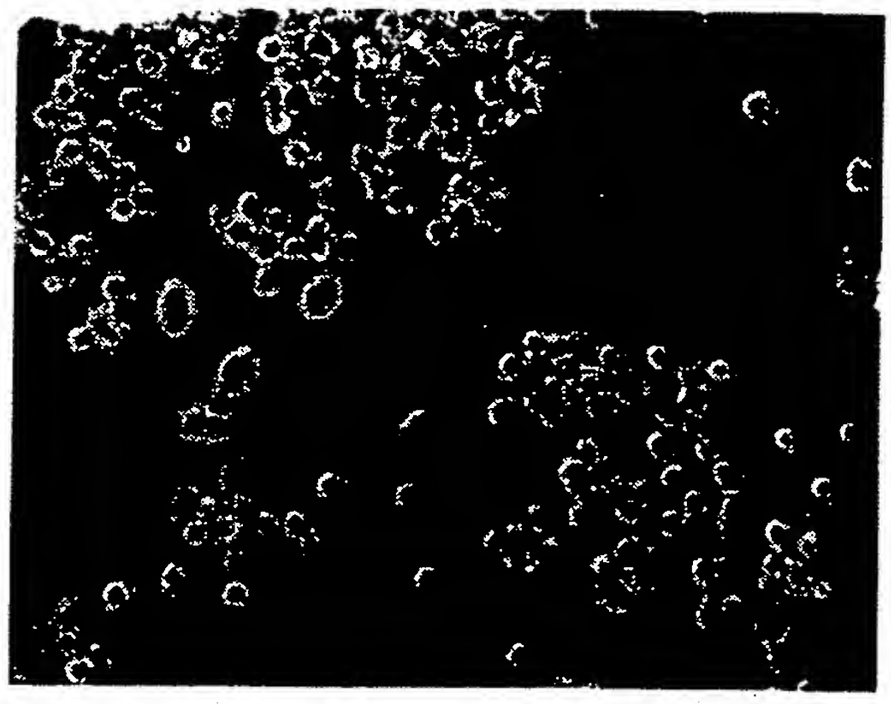


FIG. 7D

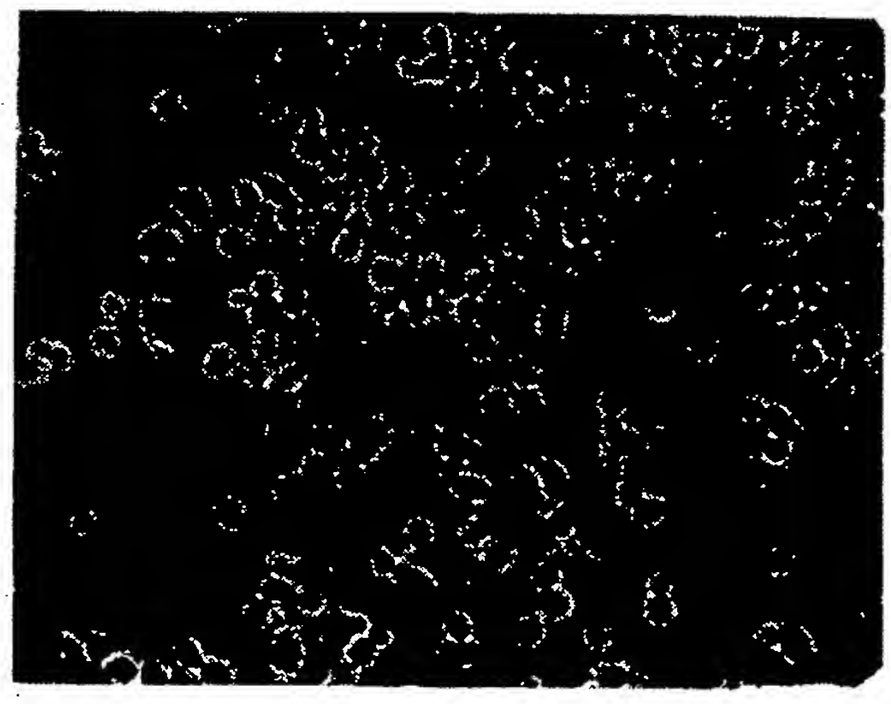


FIG. 8A

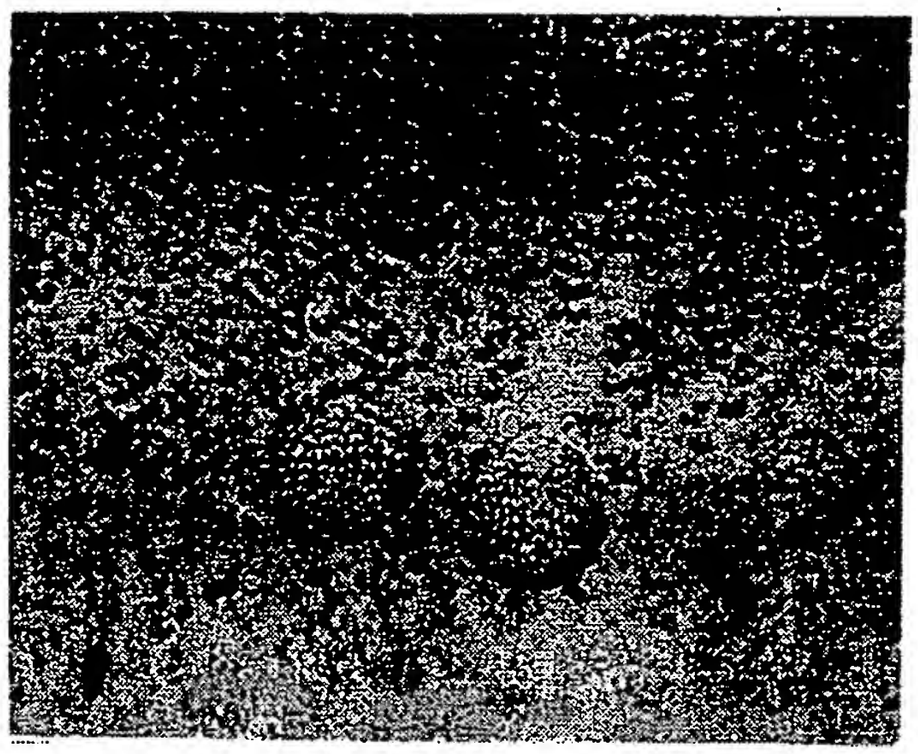


FIG. 8B

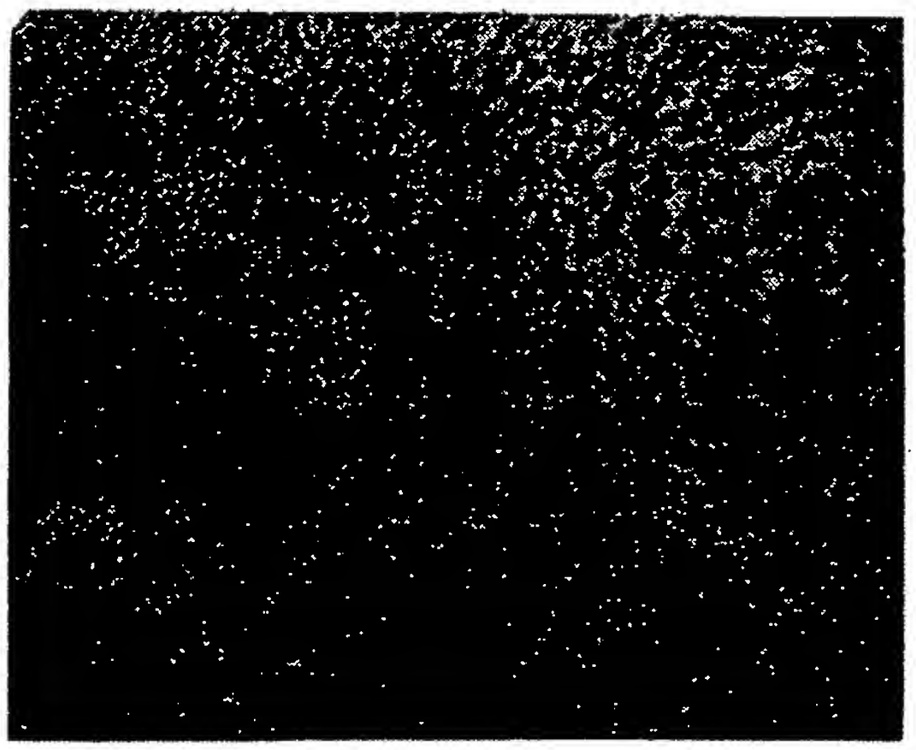


FIG. 8C

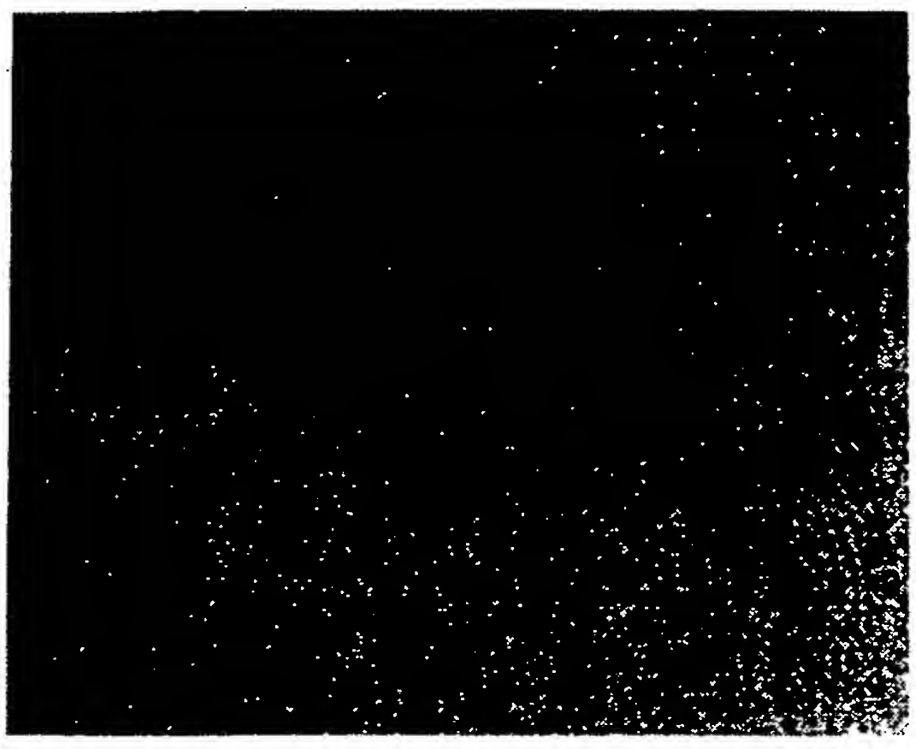


FIG. 9A

```
1    GCGGCCGCCGACGAGCCATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTG    50
                      MetValAlaGlySerAspAlaGlyArgAlaLeu

51   GGGGTCCTCAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTCATCAGCTG    100
     GlyValLeuSerValValCysLeuLeuHisCysPheGlyPheIleSerCy

101  TTTTTCCCAACAAATATATGGTGTTGTGTATGGGAATGTAACTTTCCATG    150
     sPheSerGlnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisV
      +1
151  TACCAAGCAATGTGCCTTTAAAAGAGGTCCTATGGAAAAAACAAAAGGAT    200
     alProSerAsnValProLeuLysGluValLeuTrpLysLysGlnLysAsp

201  AAAGTTGCAGAACTGGAAAATTCTGAATTCAGAGCTTTCTCATCTTTTAA    250
     LysValAlaGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLy
                                                    +50

251  AAATAGGGTTTATTTAGACACTGTGTCAGGTAGCCTCACTATCTACAACT    300
     sAsnArgValTyrLeuAspThrValSerGlySerLeuThrIleTyrAsnL

301  TAACATCATCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACT    350
     euThrSerSerAspGluAspGluTyrGluMetGluSerProAsnIleThr

351  GATACCATGAAGTTCTTTCTTTATGTGCTTGAGTCTCTTCCATCTCCCAC    400
     AspThrMetLysPhePheLeuTyrValLeuGluSerLeuProSerProTh
                                                   +100
```

```
401  ACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATAC   450
     rLeuThrCysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleP

451  CAGAGCATTACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGT   500
     roGluHisTyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCys
                          PIM3
501  CCTATGGAGCAATGTAAACGTAACTCAACCAGTATATATTTTAAGATGGA   550
     ProMetGluGlnCysLysArgAsnSerThrSerIleTyrPheLysMetGl
                                                  +150
551  AAATGATCTTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTTA   600
     uAsnAspLeuProGlnLysIleGlnCysThrLeuSerAsnProLeuPheA

601  ATACAACATCATCAATCATTTTGACAACCTGTATCCCAAGCAGCGGTCAT   650
     snThrThrSerSerIleIleLeuThrThrCysIleProSerSerGlyHis

651  TCAAGACACAGATATGCACTTATACCCATACCATTAGCAGTAATTACAAC   700
     SerArgHisArgTyrAlaLeuIleProIleProLeuAlaValIleThrTh
                                                  +200
701  ATGTATTGTGCTGTATATGAATGGTATGTATGCTTTTTAAAACAAAATAG   750
     rCysIleValLeuTyrMetAsnGlyMetTyrAlaPhe

751  TTTGAAAACTTGCATTGTTTTCCAAAGGTCAGAAAATAGTTTAAGGATGA   800
801  AAATAAAGTTTGAAATTTTAGACATTTGAAAAAAAAAAAAAAAAAAAAA   850
851  AAAAAGCGGCCGC                                       863
```

FIG. 9B

FIG. 10A

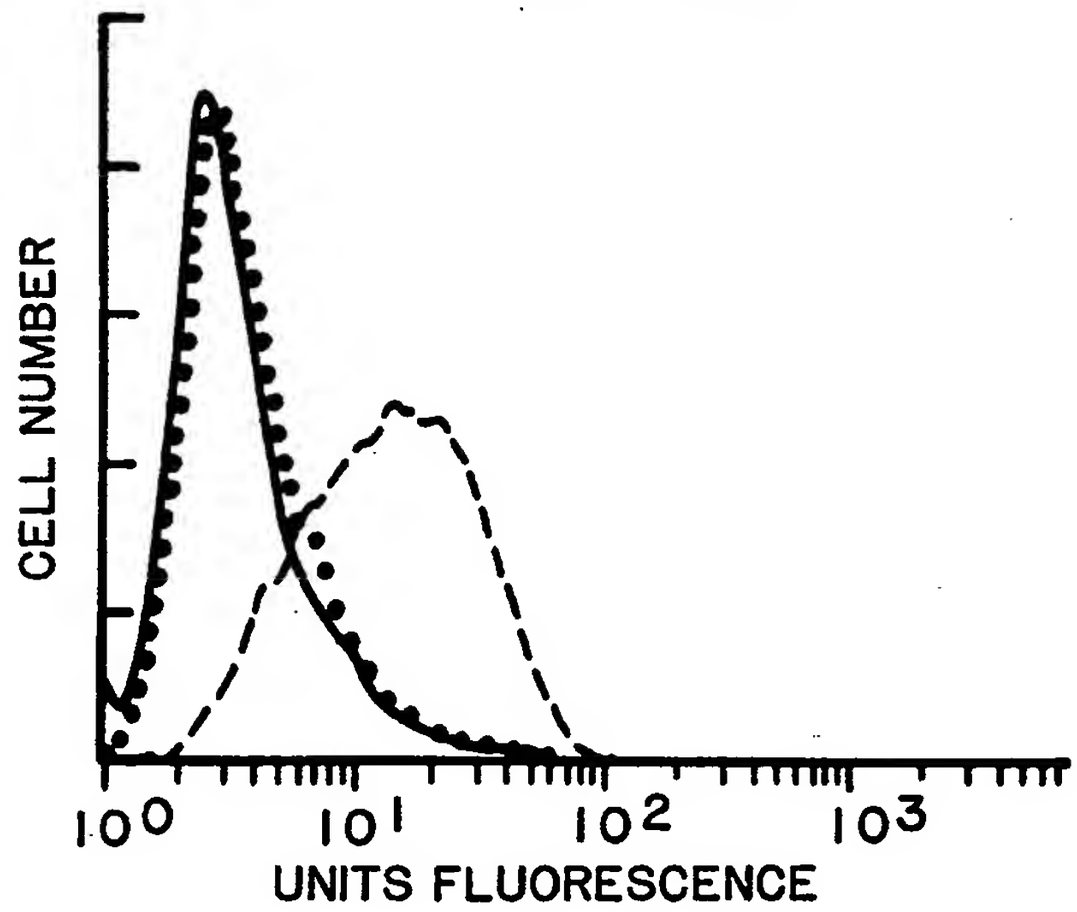


FIG. 10B

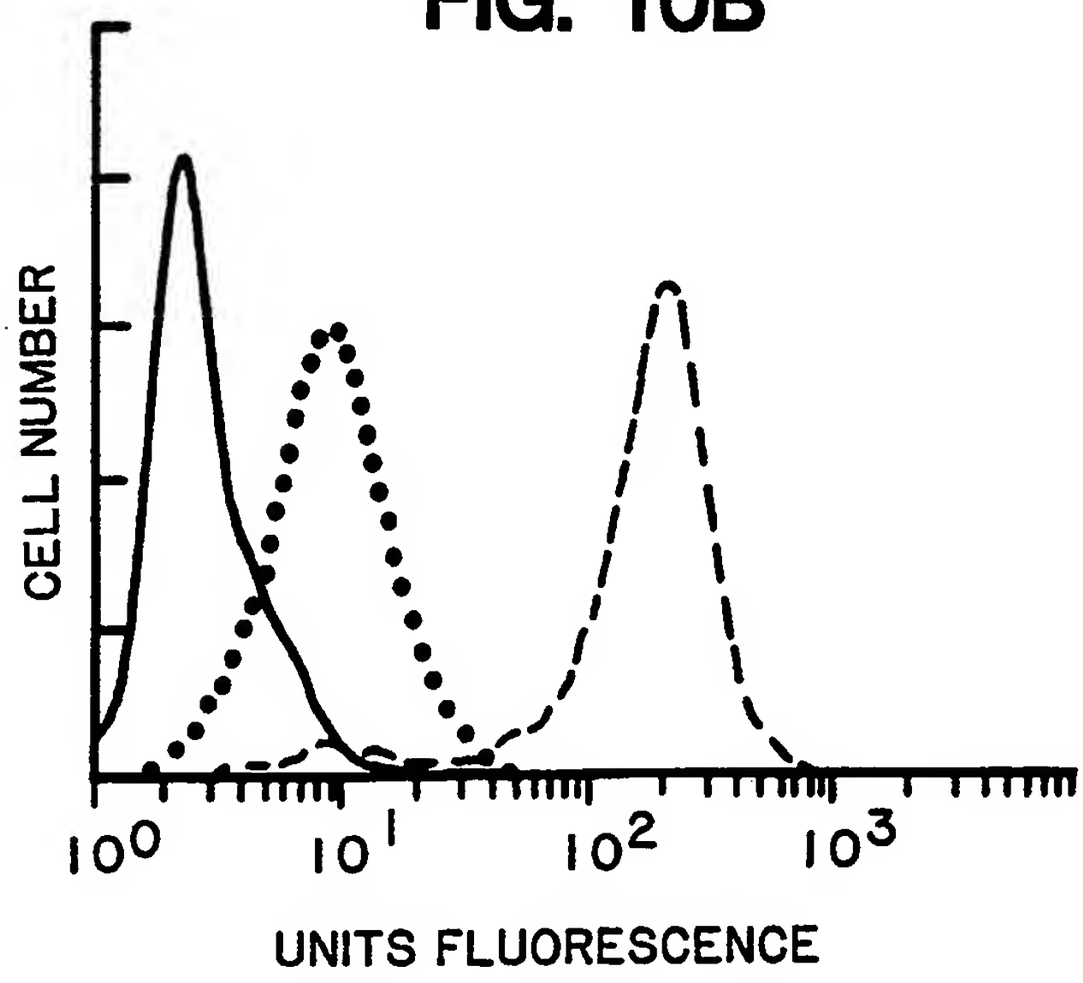
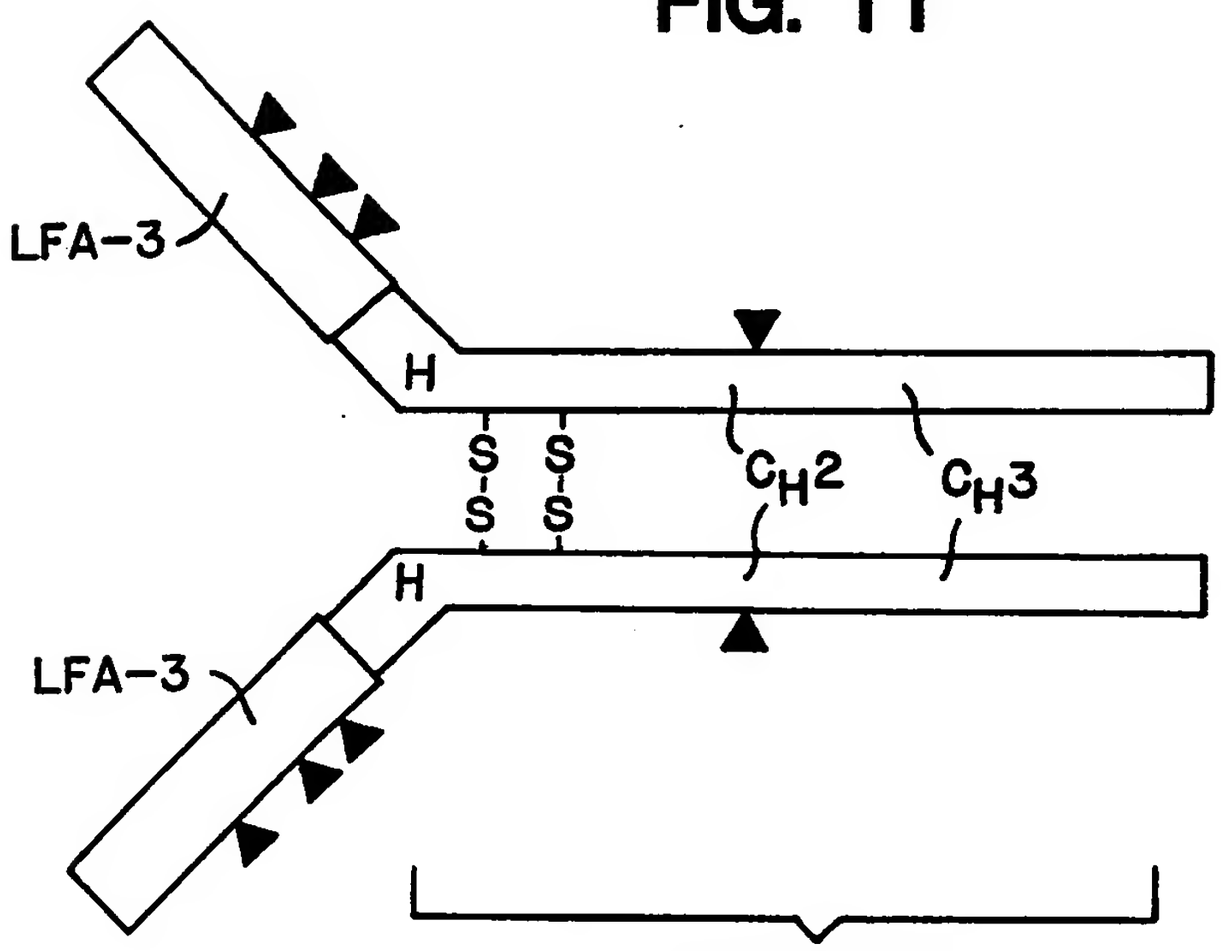


FIG. 11



HUMAN IgGI

FIG. 12A

LFA-3

```
1    ATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCTCAGCGTGGT   50
     MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLeuSerValVa

51   CTGCCTGCTGCACTGCTTTGGTTTCATCAGCTGTTTTTCCCAACAAATAT  100
     lCysLeuLeuHisCysPheGlyPheIleSerCysPheSerGlnGlnIleT

101  ATGGTGTTGTGTATGGGAATGTAACTTTCCATGTACCAAGCAATGTGCCT  150
     yrGlyValValTyrGlyAsnValThrPheHisValProSerAsnValPro

151  TTAAAAGAGGTCCTATGGAAAAAACAAAAGGATAAAGTTGCAGAACTGGA  200
     LeuLysGluValLeuTrpLysLysGlnLysAspLysValAlaGluLeuGl

201  AAATTCTGAATTCAGAGCTTTCTCATCTTTTAAAAATAGGGTTTATTTAG  250
     uAsnSerGluPheArgAlaPheSerSerPheLysAsnArgValTyrLeuA

251  ACACTGTGTCAGGTAGCCTCACTATCTACAACTTAACATCATCAGATGAA  300
     spThrValSerGlySerLeuThrIleTyrAsnLeuThrSerSerAspGlu

301  GATGAGTATGAAATGGAATCGCCAAATATTACTGATACCATGAAGTTCTT  350
     AspGluTyrGluMetGluSerProAsnIleThrAspThrMetLysPhePh
```

LFA-3 ←→ **Hinge.** ←→ **CH2**

```
351  TCTTTATGTCGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC  400
     eLeuTyrValAspLysThrHisThrCysProProCysProAlaProGluL

401  TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  450
     euLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr

451  CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAG  500
     LeuMetIleSerArgThrProGluValThrCysValValValAspValSe

501  CCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG  550
     rHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluV
```

FIG. 12B

```
551  TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC   600
     alHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyr

601  CGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA   650
     ArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLy

651  GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA   700
     sGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluL
                  CH2 ←──┬──→ CH3
701  AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC   750
     ysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThr

751  CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG   800
     LeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThrCy

801  CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA   850
     sLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerA

851  ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC   900
     snGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSer

901  GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG   950
     AspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTr

951  GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA   1000
     pGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisA

1001 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGG   1050
     snHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys
```

FIG. 13

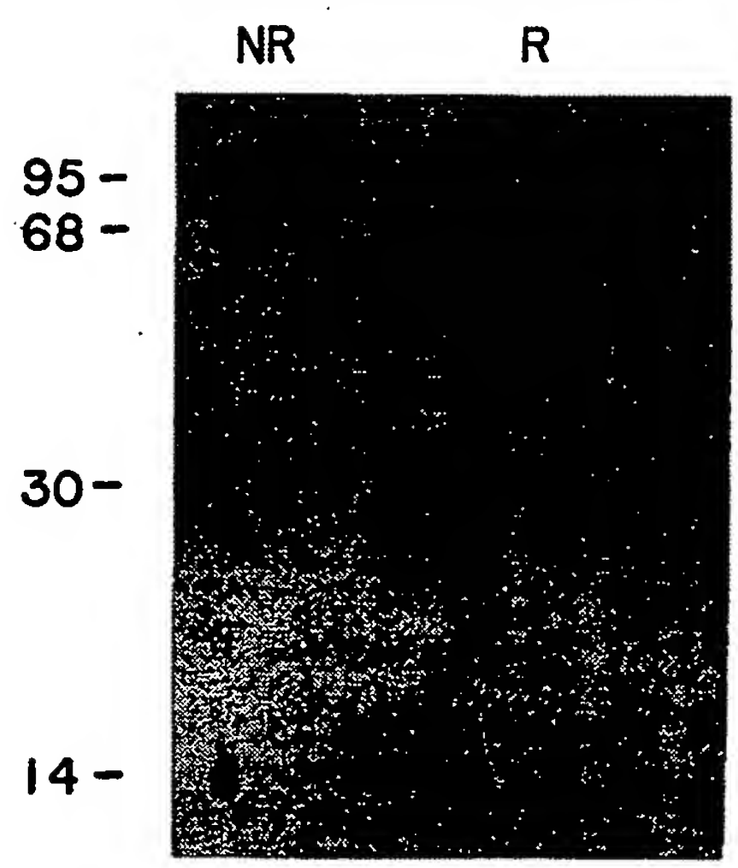


FIG. 14A

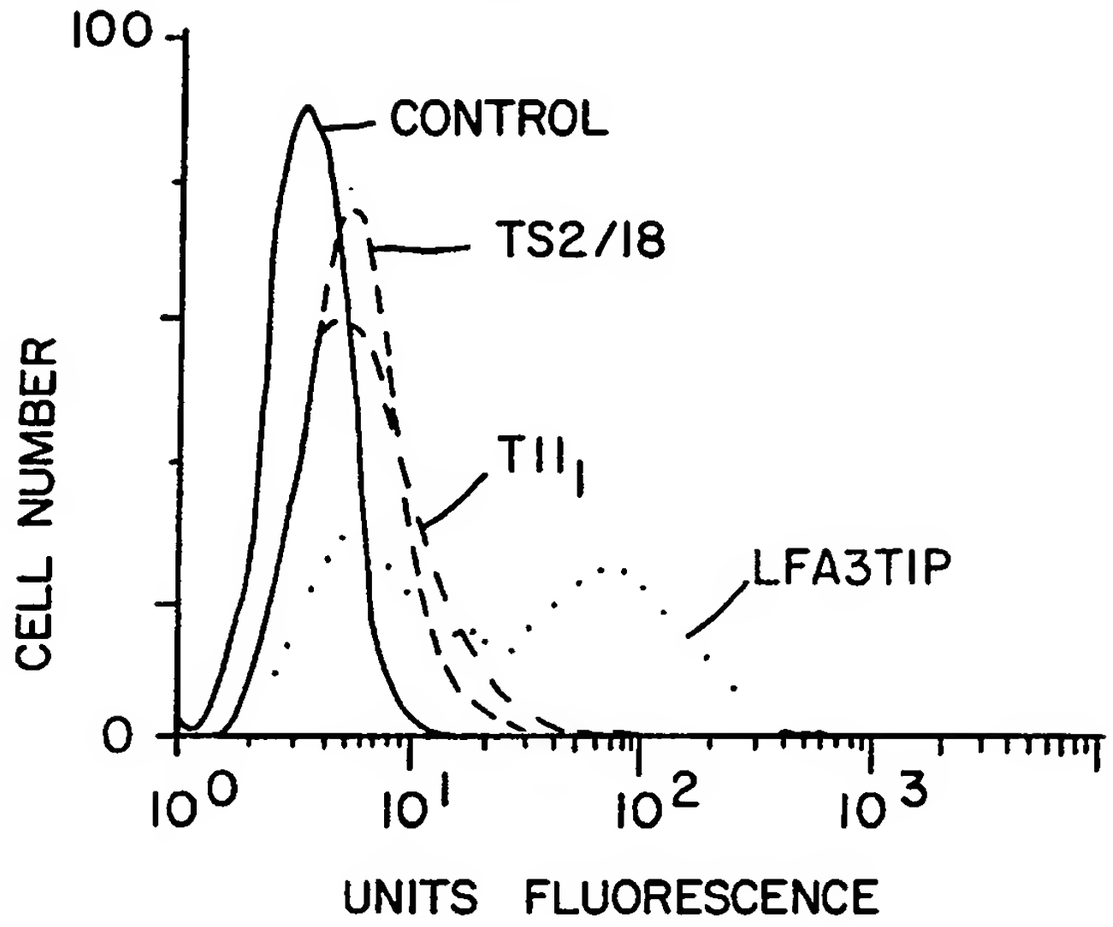


FIG. 14B

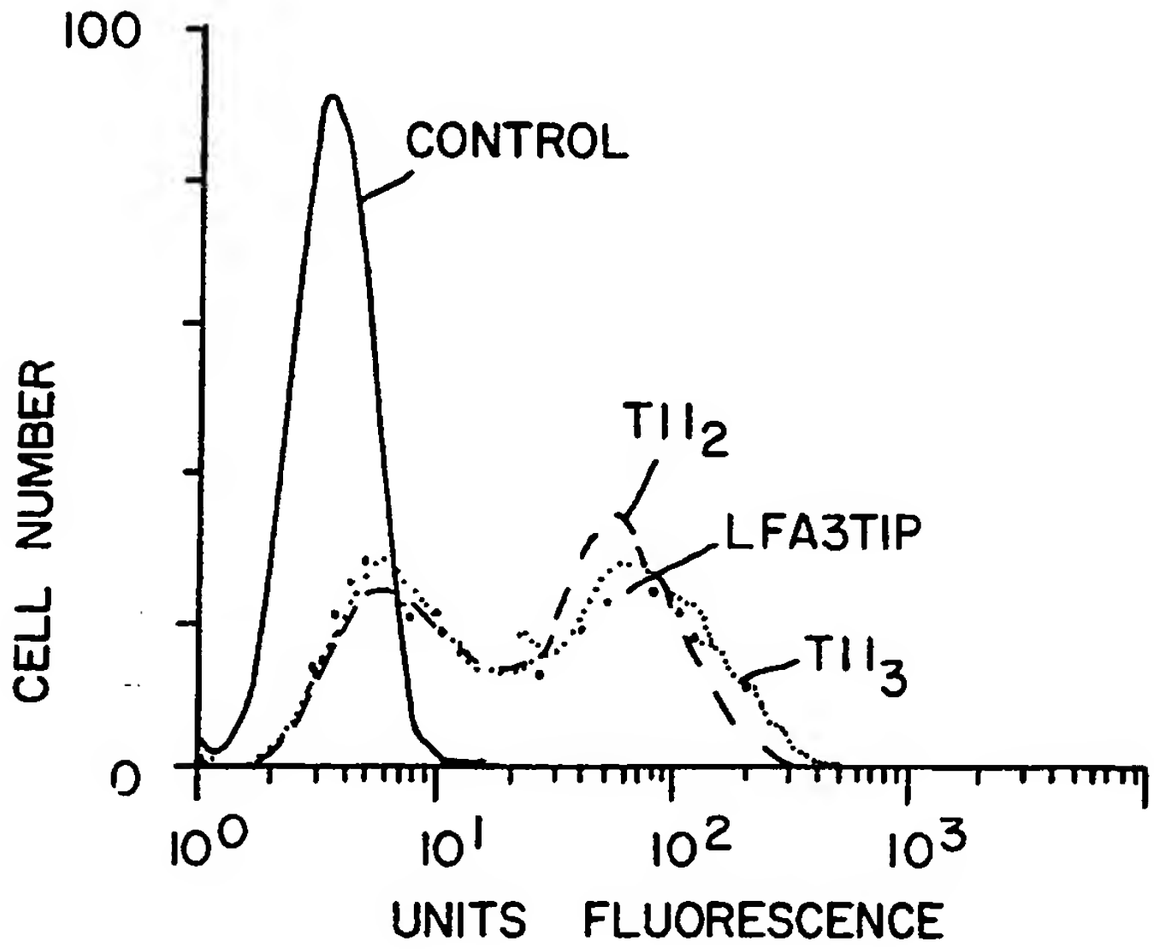


FIG. 15

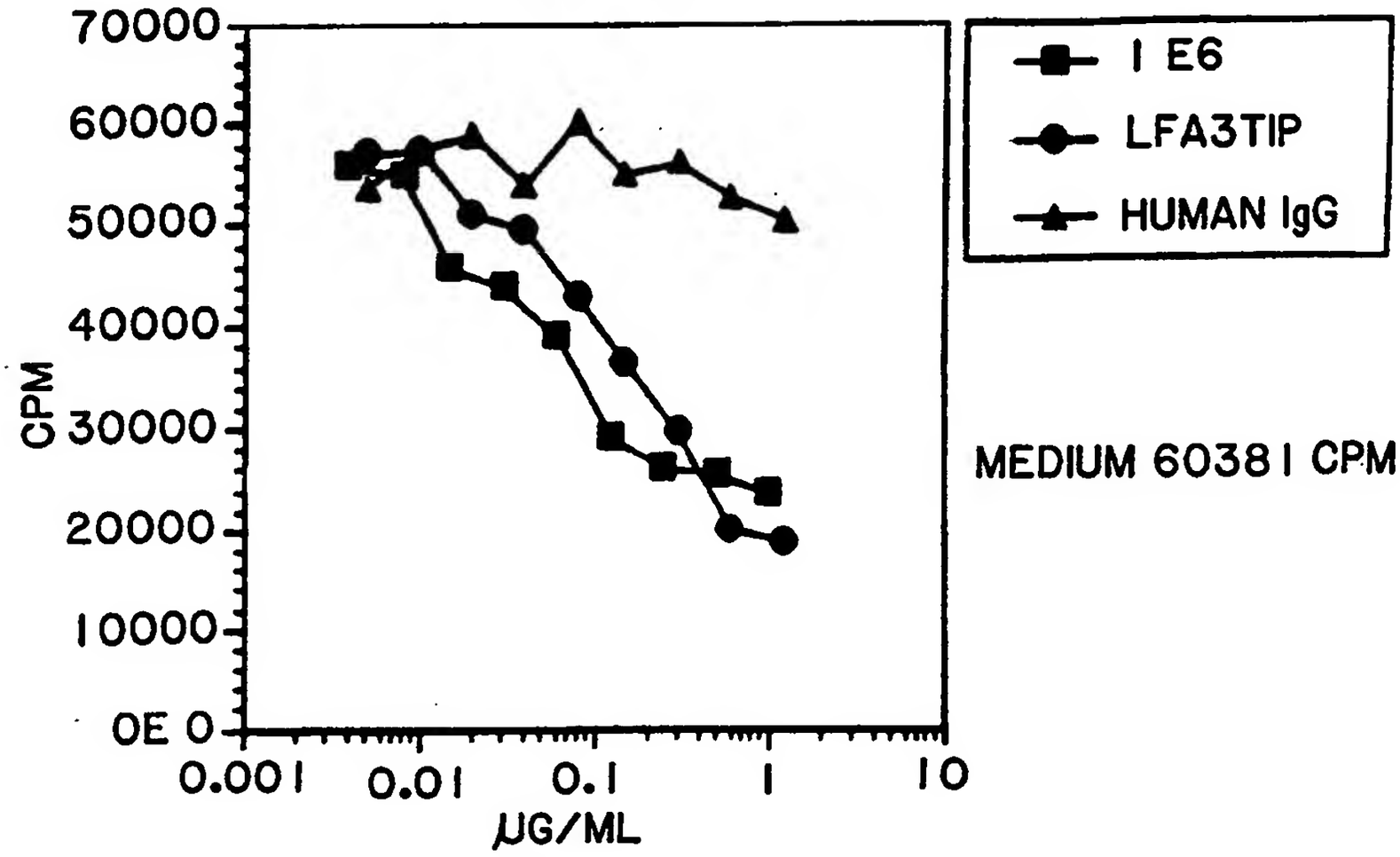

70000
60000
50000
40000
30000
20000
10000
0E 0
CPM
0.001
0.01
0.1
1
10
µG/ML
1 E6
LFA3TIP
HUMAN IgG
MEDIUM 60381 CPM

FIG. 16

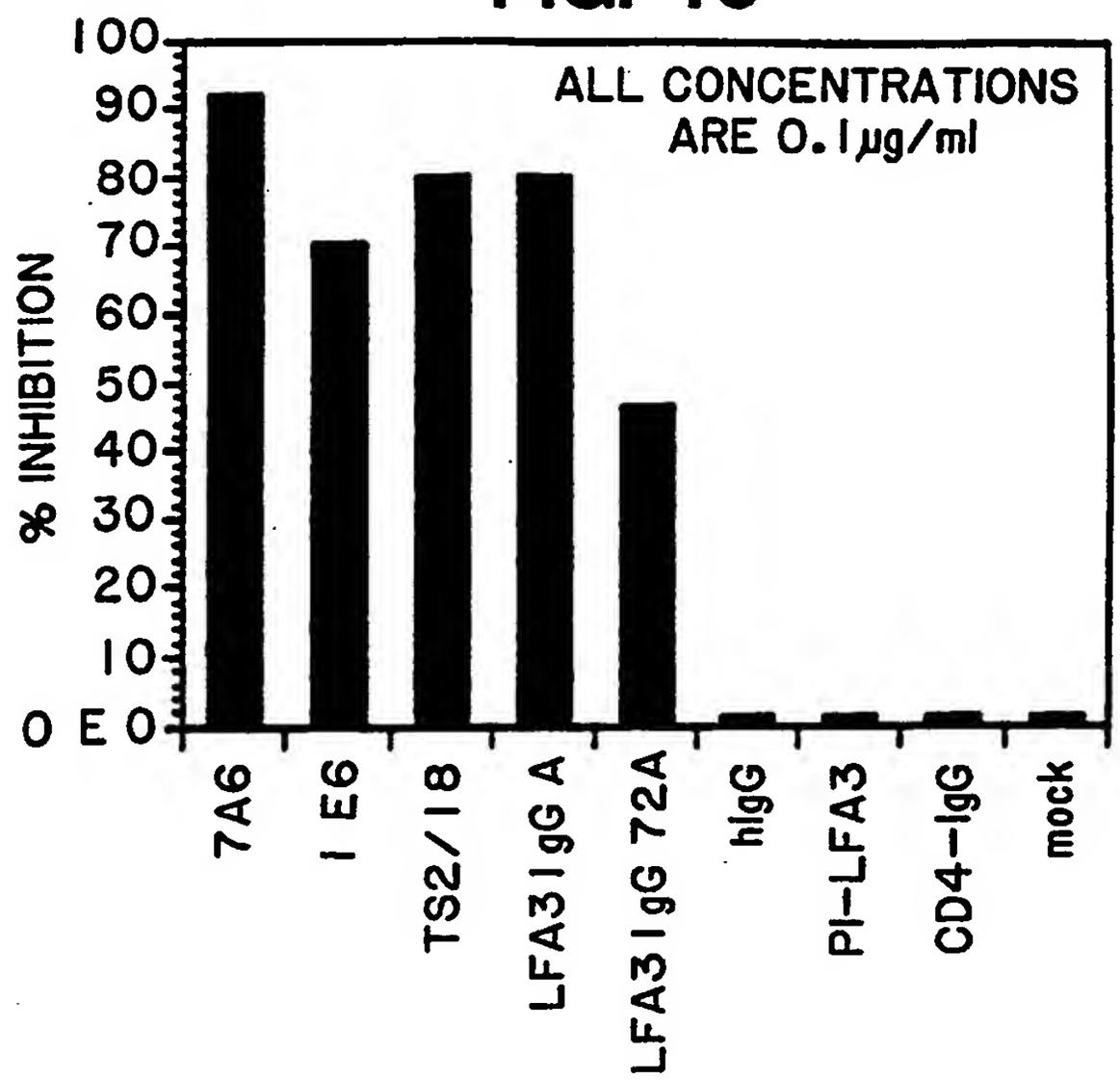
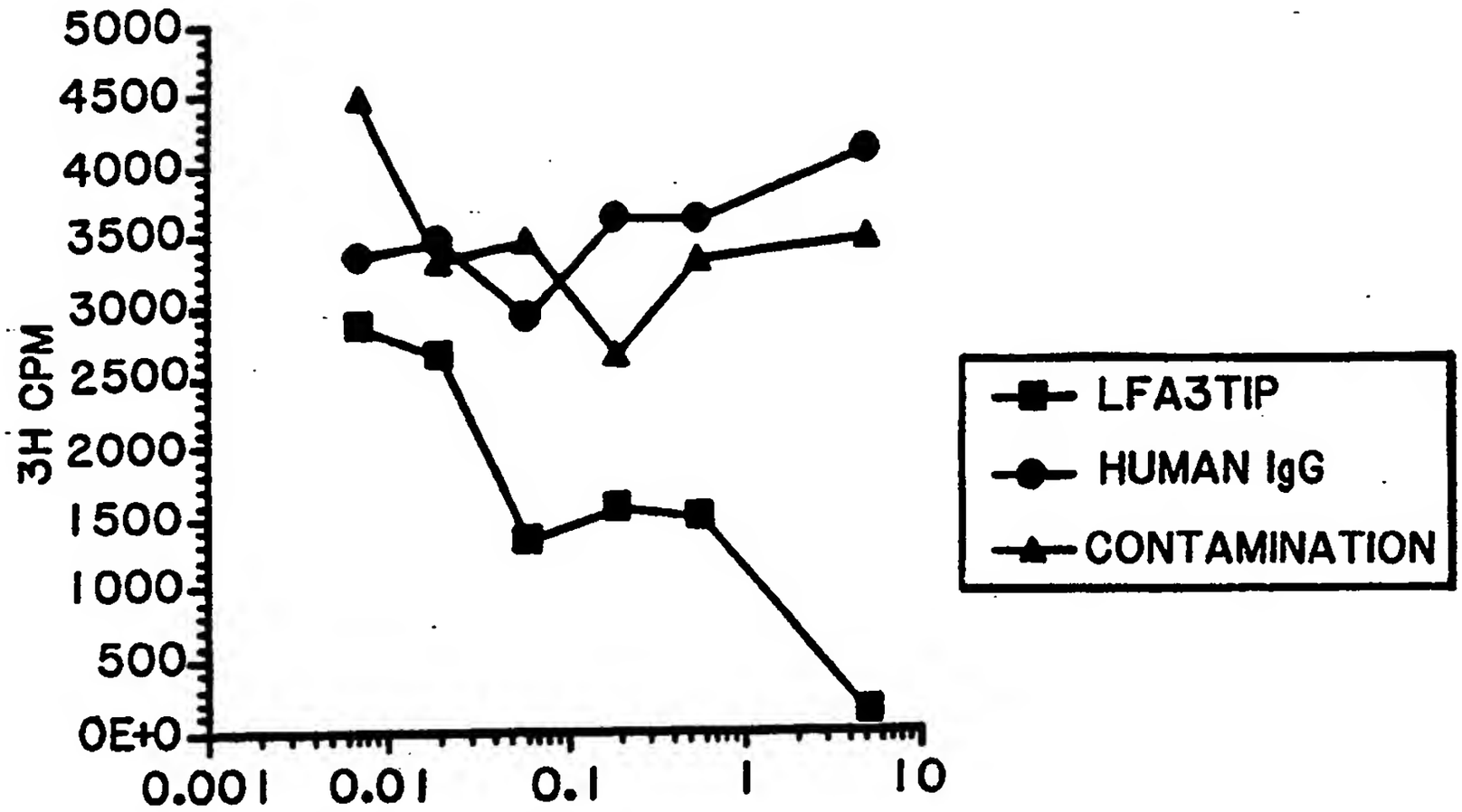

100
90
80
70
60
50
40
30
20
10
0 E 0
% INHIBITION
ALL CONCENTRATIONS
ARE 0.1µg/ml
7A6
1 E6
TS2/18
LFA3 IgG A
LFA3 IgG 72A
hIgG
PI-LFA3
CD4-IgG
mock

FIG. 17



MEDIUM 3337 cpm
T11 2+3 84936 cpm

FIG. 18

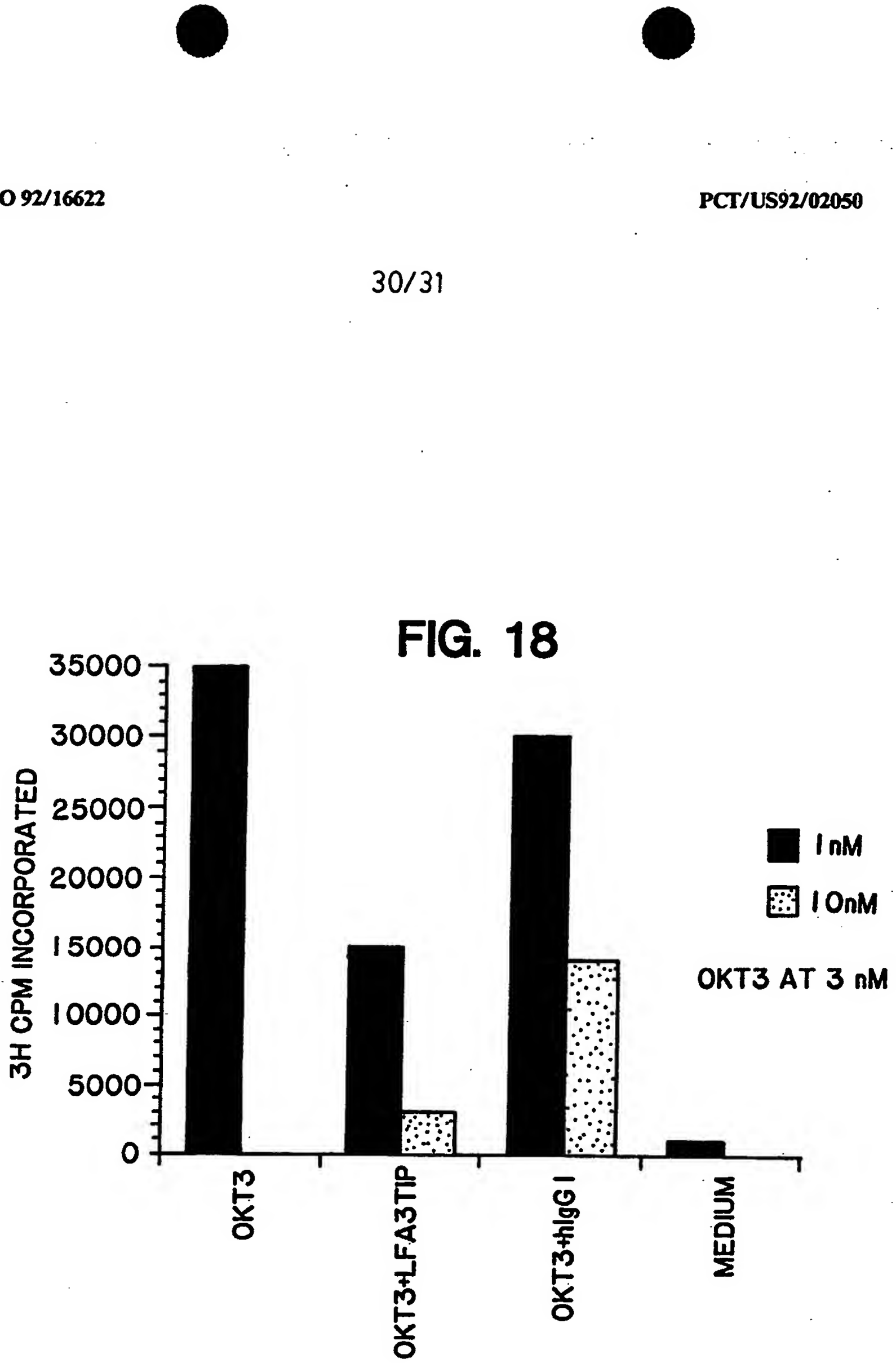
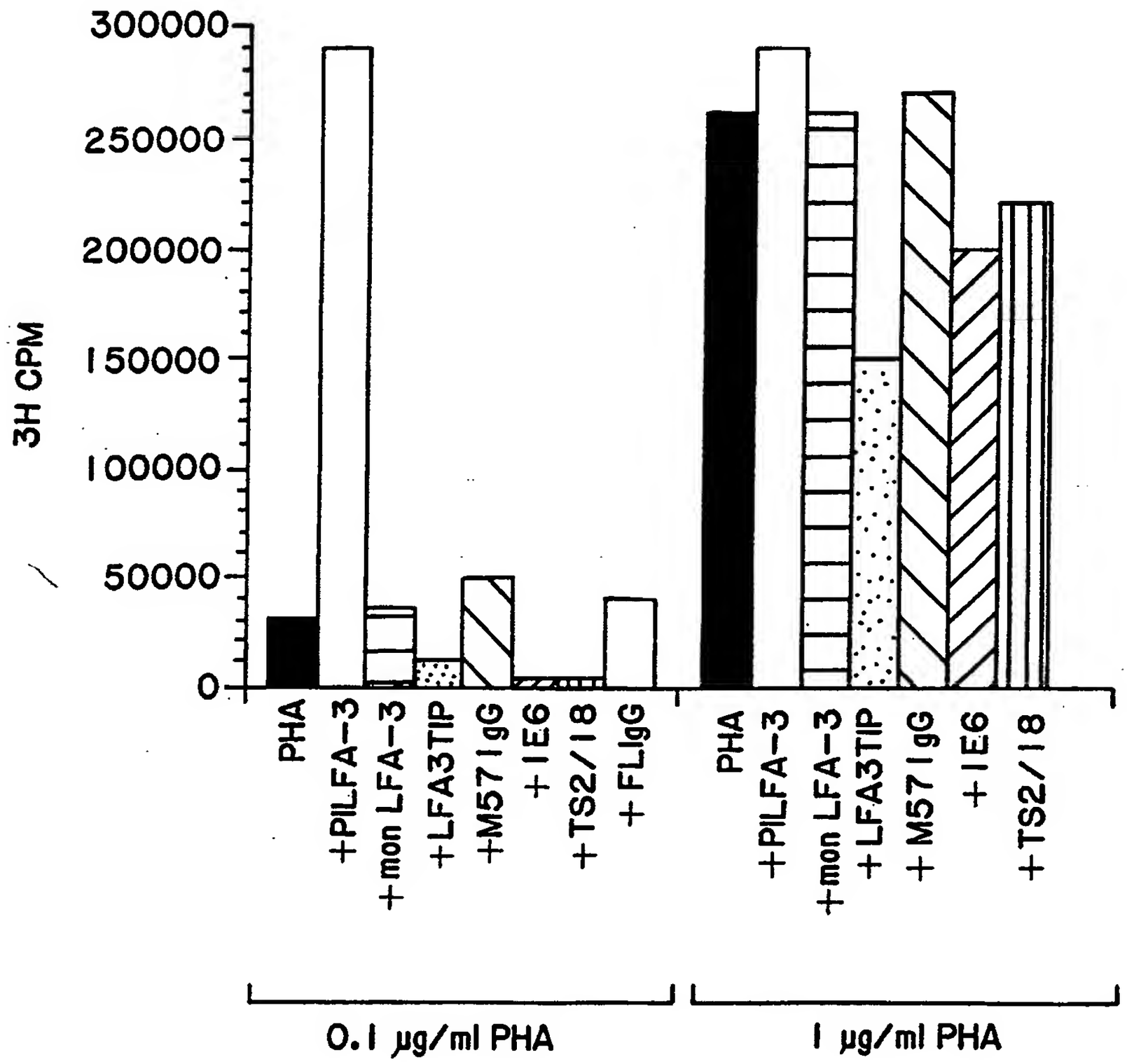

35000
30000
25000
20000
15000
10000
5000
0
3H CPM INCORPORATED
OKT3
OKT3+LFA3TIP
OKT3+hIgG1
MEDIUM
1nM
10nM
OKT3 AT 3 nM

FIG. 19


300000
250000
200000
150000
100000
50000
0
3H CPM
PHA
+PILFA-3
+mon LFA-3
+LFA3TIP
+M57 IgG
+1E6
+TS2/18
+FLIgG
PHA
+PILFA-3
+mon LFA-3
+LFA3TIP
+M57 IgG
+1E6
+TS2/18
0.1 µg/ml PHA
1 µg/ml PHA

INTERNATIONAL SEARCH REPORT

International Application No PCT/US 92/02050

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)[6]

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.Cl.5 C 12 N 15/12 C 12 N 15/62 C 07 K 13/00
C 12 N 1/21 G 01 N 33/564 G 01 N 33/566 A 61 K 37/02,39/395

II. FIELDS SEARCHED

Minimum Documentation Searched[7]

Classification System	Classification Symbols
Int.Cl.5	C 07 K C 12 N A 61 K

Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched[8]

III. DOCUMENTS CONSIDERED TO BE RELEVANT[9]

Category °	Citation of Document,[11] with indication, where appropriate, of the relevant passages[12]	Relevant to Claim No.[13]
X	WO,A,9002181 (BIOGEN, INC. USA) 8 March 1990, see the whole document (cited in the application)	1-9,18-27
Y	---	10-17
Y	EP,A,0314317 (GENENTECH, INC.) 3 May 1989, see abstract; claims; figure 3	10-17
X	--- WO,A,8809820 (BIOGEN, INC. USA) 15 December 1988, see the whole document	1-9,18-27
Y	---	10-17
X	WO,A,9012099 (BIOGEN, INC. USA) 18 October 1990, see the whole document	1-10
Y	--- -/-	11-17

° Special categories of cited documents : [10]

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
08-07-1992	12.08.92
International Searching Authority	**Signature of Authorized Officer**
EUROPEAN PATENT OFFICE	S.A. NAUCHE

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category °	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
A	DNA, vol. 8, no. 10, December 1989, Mary Ann Liebert, Inc., Publishers, (New York, US), X. WANG et al.: "A vector that expresses secreted proteins on the cell surface", pages 753-758	

ANNEX TO THE INTERNATIONAL SEARCH REPORT ON INTERNATIONAL PATENT APPLICATION NO. US 9202050 SA 59551

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on 30/07/92
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
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		JP-T-	4500905	20-02-92
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		EP-A-	0383799	29-08-90
		JP-T-	4502850	28-05-92
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		AU-A-	1955288	04-01-89
		EP-A-	0315683	17-05-89
		JP-T-	2501113	19-04-90
WO-A- 9012099	18-10-90	AU-A-	5428990	05-11-90
		CA-A-	2051694	11-10-90
		EP-A-	0466806	22-01-92